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RESULT 1
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENTS

US-09-215-694-5 ; Sequence 5, Application US/09215694B ; Patent No. 6391583 ; GENERAL INFORMATION:

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Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT : Jun A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY----ARVYPPLFYKSN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPST---PQHTHP--L 173
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                                                                                                                                                                                                                                                                                                                                                                                                                         4 PTTQKAVII-EGDKAVVKTDVSVPBLKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILG 62
               APPLICANT: Hutchinson, Charles R.
APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Park, Cheonseok n.m.i
APPLICANT: Park, Cheonseok n.m.i
TILLE OF INVENTION: WHENDO OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS
FILE REFERENCE: 960296.95718
CURRENT APPLICATION NUMBER: US/09/215,694B
CURRENT APPLICATION NUMBER: US/09/215,694B
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                        DB 4; Length 363;
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                    13.9%; Score 266.5; DB 4; 26.3%; Pred. No. 1.2e-18; tive 69; Mismatches 156;
Wisconsin Alumni Research Foundation
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RVVQGGFDHIKQGMELVRKGELSGEKLVVRL 360
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
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COMPUTER: PC
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COUNTRY: USA
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 103; Conserv
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US-09-107-532A-7298
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LENGTH: 363
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RESULT 3
US-09-328-352-8160
US-09-328-352-8160

Sequence 8160, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DATE: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 TPGTKVYGLVN------LGGYAEYA-VMPA--DRAILLPDTLD-------YVSAAG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 DVSVPELKEGTALVKVEAVAGNPTD-WKHIAYKIGPEGSILGCDIAGTVVKLGPNASTDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.5%; Score 202.5; DB 4; Best Local Similarity '27.6%; Pred. No. 3.6e-12; Matches 90; Conservative 54; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...340
SEQUENCE DESCRIPTION: SEQ ID NO: 7298:
                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-8077
INFORMATION FOR SEQ ID NO: 7298:
                          APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 ATVKFVKFINPHLNNGDIHHMNIKVF 342
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                                                     FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Acinetobacter baumannii
US-09-328-352-8160
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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APPLICANT: Taniguchi, Tadatsugu
APPLICANT: Shibuya, Hiroshi
APPLICANT: Shibuya, Hiroshi
APPLICANT: Shibuya, Hiroshi
APPLICANT: Barsoumian, Edward L.
TILLE OF INVENTION: IL-2R-Associated Polypeptides and DNA Molecules Coding Therefor FILE REPERENCE: 0652.1640000
CURRENT APPLICATION NUMBER: US/08/860,656B
CURRENT APPLICATION NUMBER: US/08/860,656B
PRIOR FILING DATE: 1996-01-15
PRIOR FILING DATE: 1995-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KOJINA, TOMOKO
APPLICANT: YAMANOTO, HIROAKI
APPLICANT: YAMANOTO, HIROAKI
APPLICANT: KAWADA, NAOKI
APPLICANT: KAWADA, NAOKI
APPLICANT: MATSUTYAMA, AKINOBU
TITLE OF INVENTION: NOVEL ENZYME, A METHOD TO PREPARE SAID
TITLE OF INVENTION: CONTAINING SAID DNA SEGMENT AND A METHOD OF PREPARING
TITLE OF INVENTION: OPTICALLY ACTIVE ALCOHOL USING SAID ENZYME
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 ASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK-N 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 VKY-FKPGDEVW-----AAVPPWKQGTLSEPVVV-------SGNBVSHKPKSLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 PESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHIN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 AYTKIVTVASKKHEKLLKSYGADDVPDYHDAGVIEQIKSKYPNLQHVIDAVG--SEDSIP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 LVKVEAVAGNPTDWK-------HIAYKIGPEGSI-LGCDIAGTVVKLGPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 158.5; DB 3
27.8%; Pred. No. 1.4e-07;
iive 39; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                       Sequence 3, Application US/08860656B Patent No. 6297028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08713254
Patent No. 5763236
                                                                                                                                                                                                                                                                                                Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 71; Conserv
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                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Sequence 2, Application US/08860656B
Patent No. 6297028
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shibuya, Hiroshi
APPLICANT: Barsoumian, Edward L.
TITLE OF INVENTION: IL-2R-Associated Polypeptides and DNA Molecules Coding Therefor File REFERENCE: 0652.1640000
CURRENT APPLICATION NUMBER: US/08/860,656B
CURRENT APPLICATION NUMBER: POT/EP95/05123
PRIOR PILING DATE: 1998-01-15
PRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                74 WKVLGWDAVGTVEAIGDKV-TQFKIGDV--VWYAGALN---RQGSNSELQLV----- 119
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                                                                                                                                                                      60 --ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKS 117
                                                                                                                                                                                                                                                    118 NLTHSTADE--ISEGPVKNFES--AASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPL 173
                                                                                                                                                                                                                                                                                                                                       174 LIWGGATAVGOQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHD--AGVIEQI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 ASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK-N 134
                                                                                                                           15 MKAVAYOKAGPITLPEALVDIBLDTPVAKGHDLLVRVQAVSVNPVDTK-IRKNVSAEQSG 73
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                                               45;
    Length 350;
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27.8%; Pred. No. 1.4e-07;
tive 39; Mismatches 96; Indels
Query Match 9.0%; Score 173.5; DB 4; Length Best Local Similarity 29.4%; Pred. No. 3.4e-09; Matches 77; Conservative 34; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       232 KSKYP-----NLQHVIDAV 245
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ORGANISM: Human p43
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NOVEL ENZYME, A METHOD TO PREPARE SAID LENZYME, A DNA SEGMENT ENCODING SAID ENZYME, A DNA SEGMENT ENCODING SAID ENZYME, A TRANSFORMANT CONTAINING SAID NAS SEGMENT AND A METHOD OF PREPARING OPTICALLY ACTIVE ALCOHOL USING SAID ENZYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 EGSILGCDIAGTVVKLGPNASTDLKVGDT-----GFGFVHGASQTDPKN---- 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 GLGYDGGYQQYLLVTRP----YRISR-IPDNVSAD----VAAAASTDAVLTP----YH 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSVPTTQKAVIIEGDKAV-VKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYK---IGP
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                     TITLE OF INVENTION: NOVEL ENZYME, A METHOD TO PREPARE SAI TITLE OF INVENTION: ENZYME, A DAA SEGMENT ENCODING SAID ETITLE OF INVENTION: OPTICALLY ACTIVE ALCOHOL USING SAID ETITLE OF INVENTION: OPTICALLY ACTIVE ALCOHOL USING SAID ENCRESPONDENCES: 11
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: P.C.
                                                                                                                                                                                                                              1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                             ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.0%; Score 153.5; DB 3;
Best Local Similarity 24.8%; Pred. No. 3.5e-07;
Matches 101; Conservative 50; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 5-337191
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-181308
FILING DATE: 02-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Oblon, No. 6255092man F. REGISTRATION NUMBER: 24,618
REFERENCE DOCKET NUMBER: 6423-TELECOMMUNICATION INFORMATION:
AKINOBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703) 413-3000
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                   CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-855-767-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ----GAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHH 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 YGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVFMT 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 -ETLPESISPGS-----FSACFDFVSVQAT-FDVCQKYVEPKGVIMPVGLGAPNLSF 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.0%; Score 153.5; DB 1; Length 336;
Best Local Similarity 24.8%; Pred. No. 3.5e-07;
Matches 101; Conservative 50; Mismatches 125; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 NNGDIHHMNIKVF-----SNGLDDVPALTEGIKEGKNKNVKYVARL 370
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PatentIn Release #1.0, Version #1.25
                                     CARGARIA PEDLICANION DIANA
APPLICATION NUMBER: US/08/713,254
FILING DATE: 12-SEP-1996
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/311,328
FILING DATE: 23-SEP-1994
APPLICATION NUMBER: UP 5-261649
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 5-337191
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-181308
FILING DATE: 02-AUG-1994
ATYONEY, AGENT INFORMATION:
NAME: Oblon, NO: 5763236man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08855767
Patent No. 6255092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YAMAMOTO, HIROAKI
KAWADA, NAOKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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APPLICANT: KOJIMA, TOMOKO
APPLICANT: YAMAMOTO, HIROP
APPLICANT: KAWADA, NAOKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 336 amino acids
amino acid
                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-713-254-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
SOFTWARE:
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Sequence 5838, Application US/09107532A
Sequence 5838, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                               71 KLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEG 130
                                                                                                                                                                                                                                                                                                                                                                                            71 ELGPGCOGHWKIGDTAMALLPGGGO-----AQYVTVPEGLLM------PIPEG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                            131 PVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 GPENLYVKEVAKPSPGEGEVLIKVAASALNRADLMQRQGQYDPPGASNILGLEASGHVA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 KHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIE-QIK-SKYPNLQHVIDAVG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP---EGSILGCDIAGTVV
                                                                                                                                                                                               35,
                                                                                                                                                  Length 322;
                                                                                                                                                                                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                             Query Match 7.8%; Score 149.5; DB 4; Best Local Similarity 26.9%; Pred. No. 8.3e-07; Matches 64; Conservative 34; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ariniello, Pamela Deneke
RRGIGYRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-5007
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INFORMATION FOR SEQ ID NO: 5838:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
                              LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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US-09-107-532A-5838
                                                                                                  US-09-154-750A-81
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  SEQ ID NO 81
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Patent No. 6380370
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-03
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-06-14
NUMBER: OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 SNLTHSTADEISEGPVK-NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLI 175
220 -ETLPESISPGS------FSACPDFVSVQAT-FDVCQKYVEPKGVIMPVGLGAPNLSF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 EGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 WGGATAVGQQLIQVAKHINAYTKIVTVASKKHE-KLLKSYGADDVFDYHDAGVIEQIKSK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 APRVLGFDAVGVIEKIGDQVSM-FQEGDVVF----YSGSPNQNGSNEEYQLIEEYL--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TMKAI---GFKSSFQLDEGNCFEEFNFDIPHPSGHELLVKVQSISVNPVDTKQRTMPVDK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TOKAVIIEGDKAVVKTD-----VSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.9%; Score 151.5; DB 4; Length 340; Best Local Similarity 27.8%; Pred. No. 5.7e-07; Matches 67; Conservative 33; Mismatches 102; Indels 39
                                                                         330 NNGDIHHMNIKVF----SNGLDDVPALTEGIKEGKNKNVKYVARL 370
                                                                                                    270 NLGDLALREIRILGSFWGTTNDLDDVLKL---VSEGKVKPVVRSAKL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81, Application US/09154750A
Fatent NO. 6492640
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
APPLICANT: Edlyak, Kornelia
TITLE OF INVENTION: p53-Induced Apoptosis
FILE REFERENCE: 1107.75357
CURRENT APPLICATION NUMBER: US/09/154,750A
CURRENT FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                          RESULT 8
US-09-134-001C-3258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 Y 235
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US-09-154-750A-81
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DEPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19274
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 ----ISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIG----PEGS--ILGCDIAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0%; Score 134; DB 4; Length 401;
11.3%; Pred. No. 4.5e-05;
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                                                                                                                                                                                                    181 TGLNVIGTASRAETQAWVRDLGAHHVID-HGKPLAEELK 218
                                                                                                                                                194 NAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 21.3%; Pred. No. 4.5e
Matches 73; Conservative 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19274, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
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APPLICANT: KOSAN BLOSCIENCES, Ir
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIER
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KHOSLA, CHAITAN
SANTI, DANIEL
WU, KAI
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US-09-410-551B-72
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APPLICANT:
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
SEQ ID NO 16756
LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFABYARVYPPLFYKSN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 VGIKEPLDIGVWKNQSISFDWEYMF------AKTDYNYEIETQGEALAHİA 300
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                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                        / Match 7.3%; Score 141; DB 4; Length 349; Local Similarity 22.5%; Pred. No. 6.9e-06; nes 89; Conservative 52; Mismatches 148; Indels 106;
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, NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...349
; SEQUENCE DESCRIPTION: SEQ ID NO: 5838:
US-09-107-532A-5838
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Best Local Similarity
Matches 59; Conserva
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US-09-252-991A-16756
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUPANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5285
LENGTH: 370
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                                                                                                                                                                                                                                                                                               219 TFAIQVMKAWGAH--VTAVCSKDASELVRKLGADEVIDYTLGSVEGLKS-LKLCAFILD 275
                                                                                        -----ALILGASGGVG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ------PDIGRLK 182
        75 IIKVHAASVNPIDVNMRSGYGATALNMKRDPLHMKTK-GEEFPLTLGRDVSGVVMECG-- 131
                                                                                                                                                              133 K-NFESAASLP-VSLT-----TAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVG 183
                                                                                                                                                                                                                                                                 184 QQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVID 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 YPPLFYKSNLTHSTADEISEGPVK-NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQ 168
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APPLICANT: Hutchinson, Charles R.
APPLICANT: Hutchinson, Charles R.
APPLICANT: Rennedy, Jonathan n.m.i.
APPLICANT: Rennedy, Jonathan n.m.i.
APPLICANT: Rarnedy, Jonathan n.m.i.
APPLICANT: Park, Cheonseok n.m.i.
TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS
FILE REFERENCE: 960296.95718
FULE REFERENCE: 960296.95718
CURRENT APPLICANTION NUMBER: US/09/215,6948
CURRENT APPLICANTON NUMBER: 1999-12-18
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
                                                           76 ASTDLKV----GDTGFGFVHGASQTDPKNGAPABYARVYPPLFYKSNLTHSTADEISEGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 ---- PEG--SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFABYARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSVPTTQKAV--IIEGDKAVVK---TDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.8%; Score 130.5; DB 4; Length 370;
Best Local Similarity 26.3%; Pred. No. 8.9e-05;
Matches 57; Conservative 33; Mismatches 78; Indels 49
                                                                                                                                                                                            172 SLTHTQAASLPYVALTAWSAINKVGGLSDRNCKGKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 HTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5285, Application US/09328352
Patent No. 6562958
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Patent No. 6391583
GENERAL INFORMATION:
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US-09-328-352-5285
                                                                                                                                                                                                                                                                                                                                                                        244 AVG 246
                                                                                                                                                                                                                                                                                                                                                                                                                           276 NVG 278
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Patent No. 6297028

Patent No. 6297028

Patent No. 6297028

Patent No. 6297028

GENERAL INFORMATION:
APPLICANT: Taniguchi, Tadatsugu
APPLICANT: Shibuya, Hiroshi
APPLICANT: Barsoumian, Edward L.
TITLE OF INVENTION: IL-2R-Associated Polypeptides and DNA Molecules Coding Therefor FILE REFERENCE: 0652.164000

CURRENT APPLICATION NUMBER: 1958-01-15

PRIOR APPLICATION NUMBER: PCT/EP95/05123

PRIOR APPLICATION NUMBER: PCT/EP95/05123

PRIOR APPLICATION NUMBER: PCT/EP95/05123

PRIOR APPLICATION NUMBER: PCT/EP95/05123

PRIOR APPLICATION NUMBER: PCT/EP95/05123

PRIOR APPLICATION NUMBER: PCT/EP95/05123

PRIOR APPLICATION NUMBER: PCT/EP95/05123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4804 TDRRLLGRMPDGWTFPQAASVMTAFATAWYGLVDLAGLR----PG-----EKVLJHAAAT 4854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 NASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VIDAVGSE--DSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITL-LYRAS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGCDIAGTVVKLGP
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6.8%; Score 131.5; DB 3; Length 396;
Best Local Similarity 27.6%; Pred. No. 7.8e-05;
Matches 67; Conservative 31; Mismatches 76; Indels 69
CURRENT APPLICATION NUMBER: US/09/410,551B
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 72
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptomyces hygroscopicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 LVKVEAVAGNPTDWK--
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ORGANISM: Mouse p43
                                                                                                                                                                                                                                                                                                                                                                  US-09-410-551B-72
                                                                                                                                                                                                                                                                                          LENGTH: 6396
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LENGTH: 396
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APPLICANT: Steinbuchel, Alexander
APPLICANT: Steinbuchel, Alexander
APPLICANT: Friefert, Horst
APPLICANT: Friefert, Horst
APPLICANT: Rabenhorst, Jurgen
TITLE OF INVENTION: SYNTHELIC ENZYMES FOR THE PRODUCTION OF CONIFERYL
TITLE OF INVENTION: ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND
TITLE OF INVENTION: VANILLIC ACID AND THEIR USE
FILE REFERENCE: Bayer-9998-CAO
CURRENT APPLICATION NUMBER: US/08/976,063E
CURRENT FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-11-29
NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AEYARVYPPLFYKSN-----LTH---STADEISEGPVKNFESAASLP--VSLTTAGVS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 ENHC---PGMIFTYNSVDRDGTRTHGGYSSMVVVHERFVVRFPDAMPLDKGAPLLCAGIT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | :: | :: | :: | :: | 1.29
176 VY----SPMKYHGLNAPGMHLGVL--GLGGLGHVAVKFGKAFGMKVTVISSSPGKKQEAL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 PATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASG-----QEILLGATRFPASPEYHEA 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 DWKHIAYKIGPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFG-FVHGASQTDPKNGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 DWKNAKYPMIP----GHEIAGEVTEVGKAV-TKFKAGDRVGVGCMVNSCQSCESCDKGF
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                                                                                                                                                                                                                            APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fader, Gary M.
APPLICANT: Fader, Gary M.
APPLICANT: Rafalbki, Antoni
TITLE OF INTERNATION: Plant Cinnamyl-Alcohol Dehadrogenase Homologs
FILE REFERENCE: BB1328 US NA
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,585
EARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 48
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Best Local Similarity 22.0%; Pred. No. 0.00036;
Matches 74; Conservative 54; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 GAEYVNTAMERLAKADVRYRFVIDIANTLDKAAAAT 369
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Patent No. 6524831
                                                                                                                                      US-09-501-115-14
; Sequence 14, Application US/09501115
; Eatent No. 6552249
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Triticum aestivum
292 LLYRASGOEIL 302
                          GENERAL INFORMATION:
APPLICANT: Steinbu
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APPLICANT:
APPLICANT:
MATC J. Rubenfield et al.
APPLICANT:
MATC J. Rubenfield et al.
TITLE OF INVENTION:
APPLICANT:
NUCLEIC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
APPLICANTON:
FILE REFERENCE:
107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                           ------HWAS 1914
                                                                                                                                                                                                                                                                                                                            61 LGCDIAGTVVKLGPNAST---DLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKS 117
                                                                                                                                                                                                                                                                                                                                                                                                                    118 NLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1966 GAGGVGQAAIILAQLTGAEVFTTAGSETKRNLLIDKFHLDPDHVFSSRDSSFVDGIKTR 2024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 FGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGP-VKNFESAASLPVSL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KS 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 GTALVKVEAVAGNPIDWKHIAYKIG----PEGSILGCDIAGTVVKLGPNASTDLKVGDTG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEVWLEQAAIGVNPLD---LGQRSGAVPIPLPSGLGLEGAGVVAALGPGVS-GLAPGD--
                                                                                                                                                                                                                                   ---KHIAYKIGP-EGSI
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                                                                                                                                        Length 2532;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.5%; Score 125.5; DB 4; Length 3
Best Local Similarity 24.4%; Pred. No. 0.00025;
Matches 76; Conservative 41; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 VTVASKKHE-KLLKSYGADDVFDYHDAGVIEQI------
                                                                                                                                      ch 6.6%; Score 126; DB 4;
1. Similarity 23.4%; Pred. No. 0.0056;
56; Conservative 39; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                      18 VVKTDVSVPELKEGTALVK--VEAVAGN--PTDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-31476
; Sequence 31476, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                           TYPE: PRT ORGANISM: Aspergillus terreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-31476
                       LENGTH: 2532
                                                                                        US-09-215-694-10
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SEQ ID NO 10
                                                                                                                                      Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
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292 GGQGVDVIYDPVGGE-LFEBAFRSIAWNGRMLVVGPASGSIPSLPANLTLLKGASLVGVF 350
                                                   GGATAVGQQLIQVAKHINAYTKIVTVASKKHE-KLLKSYGADDVFDYHDAGVIEQIKSKY 235
                                                                           236 --PNLQHVIDAVGSEDSIPEAYKVTA--------DSLPA--TLLE---VVPMT 273
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Proceedings of the National Academy of Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
ZOMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION DATA: (136)
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 94, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner. Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
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                                                                                                                                                                                                                                      274 IESIPEEIRKDNV-KIDITLLYRASGOEILLGATRPP 309
                                                                                                                                                                                                                                                                                  351 WGSFAQRQPQDNADNFRQLFAWHAEGKLKPLVSQRPP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Sacharomyces cerivisiae
FEATURE: Alcohol dehydrogenase, Table 3 Column
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
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Persson, M.
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nes 88; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: protein ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4226-4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: Alcohol
JOURNAL: Procee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                 JS-07-857-224B-94
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                                                   177
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 SNLTHSTADEISEGPVKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIW 176
                                                                                                                                                                                                                                                                                                                                                                            81 --KVGDTGFGFVHGASQTDP-----KNGAFAEYARVYPPLFYKSNLTHSTADEISE 129
                                                                                                                                                                                                                                                                                                                                                                                                                          83 GQRVASTFFPNWRAGKITEPAIEVSLGFGMDGMLAEYV----ALPYEATI------ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GPVK---NFESAASLPVSLTTAGVSLCHHLGSKMEWHPST-----PQHTHPLLIWGGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYH-----DAGVIEQIKSKY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| : | : : | : : | 231 VDLVVEVGGAGTLERSLRAVKV--GGIVATIGLVAGVGPIDPLPLISR----AlQLSGVY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 -----NVMPIPEG--MDFASAAREM---TYGTSM-HALKQRANLQPG-----ETLLVL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 PNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPM-TIESIPEEIRKDNVKIDITLLY 294
                                                                                                                                                                                                                                                                                                               8 KAVIIEG---DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHI--AYKIGPEGSIL- 61
                                                                                                                                                                                                                                                                                  26 PELKEGTALVKVEAVAGNPTDWKHIAYK----IGPEGSILGCDIAGTVVKLGPNASTDL-
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                                                                                                                                                                                      6.4%; Score 122.5; DB 4; Length 336; 24.8%; Pred. No. 0.0005; Live 54; Mismatches 115; Indels 71;
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Local Similarity 24.3%; Pred. No. 0.00087;
Hes 82; Conservative 55; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22667, Application US/09252991A Patent No. 6551795
                                                                                         TYPE: PRT
, ORGANISM: not required under old rule
US-08-976-063E-20
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US-09-252-991A-22667
                          Patentin Ver. 2.1
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                            Similarity
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SOFTWARE: Pate
SEQ ID NO 20
                                                                                                                                                                                   Query Match
Best Local Simil
Matches 79; C
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Best Local S
Matches 82
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FELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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ADDRESSEE: Dow Agrol
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CITY: Indianapolis
STATE: Indiana
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       US-07-857-224B-93
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                                                                                                                                                                      KHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSLPAT 265
                                                                                                                                                                                                                                                   EKEK--KKLGGEVFIDF-----TKTKNM-----VSDIQEATK----GGPHG 241
                                                                                                                                                                                                                                                                                            266 LLEVVPMTIESIPEEIRKDNVKIDITLLY-RASGQEILLGATRFPAS----PEYHEATVK 320
                                61 LPLVGGHEG-----AGVVVKLGSNVK-GWKVGDLAGIKWLNGSCMTCEFCESGHESNC 112
                                                                     97 -----DPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAG 149
                                                                                                         113 PDADLSGYTHDGSFQQFA------TADAIQAAKIQQGTDLAEV-APILCAG 156
                                                                                                                                              150 VSLCHHLG----SKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proceedings of the National Academy of Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Steven A. Benner STRET: Hadlaubstrasse 151
CITY: Zurich STATE: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIPICATION: 436
PRIOR APPLICATION DATA: none
TELECOWUNINICATION INFORMATION:
54 I----GPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFGFVHGASQT
                                                                                                                                                                                                                                                                                                                                                                   321 FVKFINPHLNNGDIHHMNIKVFSNGLDDVPALTEGIKE 358
                                                                                                                                                                                                                                                                                                                                                                                                       287 SINIVGSYVGNRADTREALDFFSRGLIKSPIKIVGLSE 324
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FEATURE: Alcohol dehydrogenase, Table 3 Column 16
FUBLICATION INFORMATION:
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; Sequence 93, Application US/07857224B
Patent No. 5958784
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Person, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
JOURNAL: Proceedings of Proceedings
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SEQUENCE CHARACTERISTICS:
LENGTH: 344
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DESCRIPTION:
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60 LPLVGGHEG-----AGVVVGMGENVK-GWKIGDYAGIKWLNGSCMACEYCELGNESNC 111
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                                                                                                                                                                                              59
                                                                                                                               2 SVPTTQXAVII-EGDKAVVKTDVSVPELKEGTALVKVEAVAGNPT-----DWKHIAYK
                                                                                                                                                                                       1 SIPETOKAIIFYESNGKLEHKDIPVPKPKPNELLINVKYSGVCHTDLHAWHGDWP-LPTK
Query Match 6.1%; Score 118; DB 2; Length 344;
Best Local Similarity 21.0%; Pred. No. 0.0015;
Matches 86; Conservative 52; Mismatches 147; Indel8 124; Gaps
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APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
APPLICANT: Turner, Jan R.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Broduction
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                              54 I----GPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFGFVHGASQT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 ISIVGSYVGNRADTREALDFFARGLVKSPIKVVGLSSLPEIYEKMEKĠQ 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/036,987A
FILING DATE: 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 VKFINPHLNNGDIHHMNIKVFSN-----
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09036987A Patent No. 6143526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Richard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-MAR-1998 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Stuart, Donald R REGISTRATION NUMBER: 28,47
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-----IE-----QIKSKYPNLQH-VIDAV-GSEDSIPBAYKVTADSLPATLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Saccharopolyspora spinosa
US-09-603-207-3
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09603207B
Patent No. 6521406
GENERAL INFORMATION:
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LENGTH: 2152
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-EVYATASEDKWQAVELSREHLASSRTCDFEQQFLGATGGRĞVDVVLNSLAGEFADASLR 1624
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                                                                                                                                                                                                                                                                                                                STDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFE 136
                                                                                                                                                                                                                                                                                                                                                                                  SAASLPVSLTTAGVSLCHHLGSKWEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAY 196
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Tawaford, Kathryn P
APPLICANT: Treadway, Pattl J
APPLICANT: Treadway, Pattl J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
FILE REFERENCE: 50489 DIV1
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT PILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
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                                                                                                                                                                              DB 3; Length 2152;
                                                                                                                                                                         Query Match 6.0%; Score 115.5; DB 3; Length 2 Best Local Similarity 22.6%; Pred. No. 0.05; Matches 79; Conservative 48; Mismatches 129; Indels
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6.0%; Score 115.5; DB 3;
Best Local Similarity 22.6%; Pred. No. 0.05;
Matches 79; Conservative 48; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Saccharopolyspora spinosa
US-09-370-700-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/09370700; Patent No. 6274350; GENERAL INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 amino acids
TYPE: amino acids
                                                                                                                      MOLECULE TYPE: protein US-09-036-987A-3
                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                    137
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1478 -TGLAPGDRVMGMI-----PK-----AFGPL---AVADHRMVTRIPAG--WSFA 1515 1516 RAASVPIVFLTAYYALVDLAĞLR----PG----ESLLVHBAAĞGVGMAAIQLARHLGA- 1565 1566 -EVYATASEDKWQAVELSREHLASSRTCDFEQQFLGATGGRGVDVVLNSLAGEFADASLR 1624 77 SIDLKVGDIGFGFVHGASQIDPKNGAFAZYARVYPPLFYKSNLIHSTADBISEGPVKNFE 136 77 STDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFE 136 137 SAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAY 196 9, 197 TKIVTVASK-----DHEKLLKS------YGADDVF----DYHDAGV-17 AVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILGCDIAGTVVKLGPNA 137 SAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAY 197 TKIVTVASK-----DYHDAGV------IE-----QIKSKYPNLQH-VIDAV-GSEDSIPEAYKVTADSLPATLL 93; Gaps APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/603,2078
CURRENT FILING DATE: 1990-06-23
EARLIER PLING DATE: 1990-03-09
MUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0 268 EVVPMT---IESIPEEIR----KDNVKIDITL--LYRASGQEILLGAT 306 Query Match 6.0%; Score 115.5; DB 4; Length 2152; Best Local Similarity 22.6%; Pred. No. 0.05; Matches 79; Conservative 48; Mismatches 129; Indels 93;

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RESULT 28
US-09-107-532A-5638
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1685 EPLPVTAWDVRQAPEALRHLSQARHVGKLVLTMPPVWDAAGTVLVTGGT 1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Mismatches 139;
                                                                                                                                                                                 APPLICANT: Kuhetoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9%; Score 114; 23.7%; Pred. No. 0
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APPLICATION NUMBER: US/08/804,227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Plant, Thomas, G. REGISTRATION UNBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION: TELEPHONE: 317.276-2459
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                        Sequence 10, Application US/08804227C
                                                                                                                                                                                                                                                                                                    ADDRESSEE: THOWAS G. PLANT 15
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: ASCI(DOS) Text only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: February 21,
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Floppy disk
IBM Compatible
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US-08-804-227C-10
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 85; Conserva
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                                                                                                                       Patent No. 587699
                                                                                US-08-804-227C-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches 139; Indels
                APPLICANT: Kubetoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESS:
ADDRESSES: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:|: | :: | | 3099 IARHLGA--EVLATASPGKWDALRAMGITD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Macintosh 7.0
Burgett, Stanley G.
Kuhstoss, Stuart A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.7%;
Matches 85; Conservative 40
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                            46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                COUNTRY:
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52 YKIGPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 IKSKYP-NLQHVIDAVGSEDSIPEAYKVTADSLPA-------TLLEVVPMTIE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 SIPEEIRKDNVKIDITLL----YRA-----SGO---BILLGATRFPASPEYH- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 PDIGFEG-----IGEVVALGLSASARYTVG------QAVAYMAP--GSPAEYTVVPA
                           GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Priemer. Nelson B.
APPLICANT: Friemer. Nelson B.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 1
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSER: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.8%; Score 111; DB 2; Length 300 Best Local Similarity 24.0%; Pred. No. 0.0061; Matches 80; Conservative 42; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---EATVKFVKFINPHLNNGDI-----HHMNIKV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 TGLESIFRAVNYMYMGKNTGKIVVELPHSVNSKL 300
                                                                                                                                                                                                         E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,010
FILING DATE: 27-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853-068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: COLUZI, LBURA A
REGISTRATION NUMBER: 30,742
REPRENCE/DOCKET NUMBER: 785:
TELECOMMUNICATION INFORMATION:
TELEPANONE: 212-790-9090
TELEXAX: 212-869-8864
TELEX X: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30,742
                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 amino acida
                                                                                                                                                                                                                                                                                                                 ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 27-MAR-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COROPERATING SYSTEM:
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                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                 USA
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FRAGMENT TYPE:
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Sequence 5638, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 IAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEISEGPVK-NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 EGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL-----GCD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 EAQDVFEEIDAHPREVGSGHVRVEIKAFSVNPYD---VALRLGEMKEIRTWKFPYVPGND 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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26.3%; Pred. No. 0.0018;
tive 37; Mismatches 75; Indels 45
                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 QQLIQVAKHINAYTKIVTVASKKHEKLLKSYGA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 SSLIQLLHEKG--IRILTSASSKNEEKVTKFGA 194
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-70n-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...200
SEQUENCE DESCRIPTION: SEQ ID NO: 5638:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
US-08-828-010-2
; Sequence 2, Application US/08828010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TH: 200 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 5638:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                       NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Ilnear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56; Conservative
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                                                                                                                                                                                                                                                                                            ZIP: 02354
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Matches 5
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104 AEYARVYPPLFYKSNLTHSTADE------ISEGPVKNFESAASLPVS--LTT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 REALERLGA------DAFVVSSSAEEMEAARSTMDGVINTVSANTPMAPYLALLKPNG- 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGVSLCHHLGSKWEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKH 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 EKLLKSYGADDVFDYHDAGVI----EQIKSKYPNLQHVIDAVGSEDSI------PEAY 255
RESULT 30
US-09-501-115-10
; Sequence 10, Application US/09501115
; Patent No. 6552249
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fader, Gary M.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehadrogenase Homologs
; TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehadrogenase Homologs
; FILE REPERENCE: BB1328 US NA
; CURRENT APPLICATION NUMBER: US/09/501,115
; CURRENT PILING DATE: 1999-February-10
; EARLIER PILING DATE: 1999-February-10
; SEQ ID NO 10
; LENGTH: 366
; TYPE: PRT
; ORCANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.8%; Score 110.5; DB 4; Length 366; Best Local Similarity 22.0%; Pred. No. 0.0095; Matches 57; Conservative 44; Mismatches 101; Indels 57;
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Search completed: January 10, 2004, 10:08:46 Job time : 34 Becs

Title: Perfect score:

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Scoring table:

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Sequence 6, Appli
Sequence 6, Appli
Sequence 10703, A
Sequence 10703, A
Sequence 10744, A
Sequence 10944, A
Sequence 16579, A
Sequence 8218, Ap
Sequence 8218, Ap
Sequence 8218, Ap
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Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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cgn2_6/ptodata 2 pubpa 4 USOT PUBCOMB. pep: *
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17: /cgn2_6/ptodata 2 pubpa 4 USOB PUB. PUB. pep: *
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-081-644-4

4 US-10-081-644-6

4 US-10-081-644-8

US-10-137-03-66

US-10-137-03-66

US-10-136-701-10740

US-10-156-761-8739

US-10-156-761-14981

US-10-156-761-14981

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US-10-156-761-8218

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Maximum Match 100%
Listing first 90 summaries
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                                                     protein search, using sw model
                                                                           January 10, 2004, 10:07:24
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Gapop 10.0 , Gapext
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Maximum DB seq length: 200000000
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Sequence 14785, A Sequence 6795, App Sequence 61825, App Sequence 61836, App Sequence 5102, App Sequence 5102, App Sequence 6192, App Sequence 6192, App Sequence 6192, App Sequence 2016, App Sequence 2016, App Sequence 2018, App Sequence 2018, App Sequence 2018, App Sequence 2018, App Sequence 2018, App Sequence 2018, App Sequence 2018, App Sequence 2018, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 2013, App Sequence 201

Sequence 1472, Apple Sequence 11164, A Sequence 11164, A Sequence 43, Appl Sequence 45, Appl Sequence 45, Appl Sequence 16399, A Sequence 16399, A Sequence 23041, A Sequence 23041, A Sequence 23041, A

1920 1065.5 1015.5 1015.5 265 265 207 207 201.5 197.5 193.5 186.5

Score

Result No.

Sequence Sequence Sequence

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US-10-081-644-6

Sequence 6, Application US/10081644

Sequence 10 Molication US/10081644

Sequence 6, Application US/10081644

GENERAL INFORMATION:

APPLICANT: Yamamoto, Hiroaki

APPLICANT: Yamamoto, Hiroaki

APPLICANT: Yamamoto, No. US2020192782Alihiro

APPLICANT: Kimoto, No. US2020192782Alihiro

APPLICANT: Kimoto, No. US2020192782Alihiro

APPLICANT: Wimoto, No. US2020192782Alihiro

TITLE OF INVENTION: CARBON-CARBON DOUBLE BOND OF AN ALPHA, BETA-UNSATURATED KETONE

TITLE OF INVENTION: USANG THE REDUCTASES

TITLE OF INVENTION: USANG THE REDUCTASES

FILE REFERENCE: 06501-100001

CURRENT APPLICATION NUMBER: US/10/081,644

CURRENT APPLICATION NUMBER: US/10/081,644

PRIOR PELING DATE: 2001-02-23

NUMBER OF SEO ID NOS: 29
    OF AN ALPHA, BETA-UNSATURATED KETONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GCDIAGTVVKLGPNA-STDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYK--SN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GCDAAGQIVKIGPNVDAARFAIGDYIYGVIHGASVRFPSNGAFAEYSAISSETAYKPARE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 LTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 ATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ATAVGQMLIQLAKKLNGFSKIIVVASRKHEKLLKEYGADBLFDYHDADVIEQIKKKYNNI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 PYLVDCVSNTETIQQVYKCAADDLDATVVQLTVLTEKDIKEEDRRQNVS1EGTLLYLIGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 NDVPPGTFTLPADPEYKEAAIKFIKFINPKINDGEIHHIPVKVYKNGLDDIPQLLDDIKH 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 QHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASG 298
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                                                                                                                                                                                                                                                                                                                                               DB 14; Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                            59; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                               55.5%; Score 1065.5; DB 54.0%; Pred. No. 1.2e-91
       BOND
TITLE OF INVENTION: CARBON-CARBON DOUBLE BO
TITLE OF INVENTION: USING THE REDUCTASES
FILE REFERENCE: 06501-100001
CURRENT APPLICATION NUMBER: US/10/081,644
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: JP 2001-49363
PRIOR PILING DATE: 2001-02-23
NUMBER: OF SEQ ID NOS: 29
SEQ ID NO 4
SEQ ID NO 4
    CARBON-CARBON DOUBLE USING THE REDUCTASES
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                 LENGTH: 376
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APPLICANT: Yamamanco, Hiroaki
APPLICANT: Yamamanco, No. US20020192782Alihiro
APPLICANT: Ximoco, No. US20020192782Alihiro
APPLICANT: Ximoco, No. US20020192782Alihiro
TITLE OF INVENTION: PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A
TITLE OF INVENTION: CARBON-CARBON DOUBLE BOND OF AN ALPHA, BETA-UNSATURATED KETONE
TITLE OF INVENTION: USING THE REDUCTASES
FILE REFERENCE: 06501-100001
CURRENT APPLICATION NUMBER: US/10/081,644
FILE REFERENCE: 0202-02-21
FRICH FILING DATE: 2001-49363
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PERSEC for Windows Version 4.0
SED ID NO 2.
    Sequence 22735, A
Sequence 959, App
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APPLICANT: Yamoto, No. US20020192782A1ihiro
TITLE OF INVENTION: NOVEL ENONE REDUCTASES, METHODS FOR
TITLE OF INVENTION: PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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100.0%; Pred. No. 3.7e-172;
ive 0; Mismatches 0;
    US-10-369-493-22735
US-10-238-075-959
                                                                                           ALIGNMENTS
                                                                                                                                                                                                     Sequence 2, Application US/10081644
Publication No. US20020192782A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Kluyveromyces lactis
       12
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Best Local Similarity 100.
Matches 370; Conservative
       350
1298
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67 GFSL.PAVPGYDLAGVVVKVGREVK-ELKVGDEVYGFMFHAK----KDGTLAEYAAVESSF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 SLIQLANKLNGFTKIIVVASRKHEKLLKEYGADQLFDYHDIDVVEQIKHKYNNISYLVDC 241
                                                                          242 VANQNTLQQVYKCAADKQDATVVBLTNLTEBNVKKENRRQNVTIDRTRLYSIGGHBVPFG 301
                                                                                                                           305 ATRPPASPEYHEATVKPVKFINPHLNNGDIHHMNIKVPSNGLDDVPALTEGIKEGKNKNV 364
                                                                                                                                               245 VGSEDSIPEAYKVTADSLPATILEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VPTTQKAVII--EGDKAVV---KTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 G----SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 TPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
PRIOR FILING DATE: 2001-04-30
PRIOR PILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-06-20
PRIOR PELING DATE: 2000-06-20
PRIOR PELING DATE: 2000-06-20
PRIOR PLING DATE: 2000-06-20
PRIOR PLING DATE: 2000-06-20
PRIOR PLING DATE: 2000-06-20
PRIOR PRIOR DATE: 1000-06-20
PRIOR PRIOR PLING DATE: 1000-06-20
PRIOR PRIOR PLING DATE: 1000-06-30
PRIOR PRIOR PLING DATE: 1099-07-30
PRIOR PLING DATE: 1999-07-30
PRIOR PLING DATE: 1999-01-35
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PREUSED for Windows Version 4.0
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APPLICANT: Visser, Elizabeth
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.1036-4
CURRENT APPLICATION NUMBER: US/10/137,036
CURRENT FILING DATE: 2002-04-30
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; Pred. No. 1.8e-16;
31; Mismatches 93;
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Publication No. US20030101478A1
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33.6%;
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Best Local Similarity 33.64
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Perera, Ranjan
APPLICANT: Rice, Stephen
APPLICANT: Eadleton, Clare
APPLICANT: Lasham, Annette
                                                                                                                                                                                                  365 KYVARL 370
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                                                                                                                                               NLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWG 177
                                                                                                                                                                                                                    124 ELKFLGEDVLPAGPVRSLEGVATIPVSLTTAGLVLTYNLGLDLKWEPSTPQRKGPILLWG 183
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                                                                                                                                                                                                                                                                                         LOHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRAS 297
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                                                                          VAIPETMKAVVIEDGKAVVKEGIPIPELEEGFVLIKTLAVAGNPTDWAHIDYKIGPOGSI
                                                      MSVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSI
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53.0%; Pred. No. 5.8e-87;
ive 60; Mismatches 109; Indels
   ; Pred. No. 1.6e-87;
67; Mismatches 110; Indels
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 51.7%;
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                  Matches 193; Conservative
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Best Local Similarity
Best Local Similarity
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US-10-156-761-8739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 VDLVFDTMGGEVQKNSFDVLKFNTGRLVSIVGIEDKQLAAEKNVSAESI---WLQPNGEQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 FYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 LIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQI-- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------KSKY----PNLQHVIDAVGSEDSIPEAYK-VTADSLPATLLEVVPMT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 KAVIIE--GDKAVV-KTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 IESIPEEIRKDNVKIDITLLYRASGQEILLGATRFPASPEYHEATVKFV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 LQKIADLMAAGKVKSIIGEVFPFSRQ----GIYDAHALSETHHAVGKIV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.8%; Score 265; DB 9; Length 322; 30.4%; Pred. No. 2.3e-16; Live 42; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                   APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in
ITILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
212 N-FEDLPEKF---DVVYDTVGEIERAAKAVK 238
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12.2
PRIOR PILING DATE: 2000-12.2
PRIOR PILING DATE: 2000-12.2
PRIOR PILING DATE: 2000-12.2
                                                                                                                       Sequence 10703, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                       APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                            Trawick, John D.
Carr, Grant J.
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Best Local Similarity
Matches 106; Conserv
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SEQ ID NO 10703
LENGTH: 322
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122 STADEISEGPVK-NFESAASLPVSLTTAGVSLCH----HLGSKMEWHPSTPQHTHPLLIW 176
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                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
FRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8740
                                                                                      APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SHEBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATYORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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APPLICANT: SAKAKI, YOSHITYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 NLQHVIDAVGSEDSIPEAYKV-----
Sequence 8740, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8739, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 RROAKKLGVTYEFLFMRASGDQL--
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UN
APPLICANT: HORIKAWA, HIROSHI
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61 LILGSDFAGIVVSVGKKVQ-NPRLGDAVYGRV-----PKNRVGTFABYIAVDQAAVAM 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 YKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 KPKNLT------FEEAAAIPL----VGLTSYQALHDIMNVQPG-----QKVL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 IWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKGK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 QKELAIE-----EVPLPTIHDNDVLVKIIAASINPIDLKTKDGKVKMLLNYQM---P 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 OKAVIIEGDKAVVKTDVSVPELKEGTALVKVBAVAGNPTDWKH-----IAYKIGPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 YPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLE-----VVP----MTIESIPEE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 Y---DYVFDTWG-------GTILEKAFSVVKPQGKVVTLSGIPNE 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 206; DB 9; Length 338; 28.1%; Pred. No. 8.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1e-10
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADANOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERBNCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39, Mismatches
                                            PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 10944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 201.5; 25.9%; Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14981, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
              APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptomyces avermitilis US-10-156-761-14981
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 28.1% tes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Local 80; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-815-242-10944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY----ARVYPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 LFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KPANLTH-------GER 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---QNAERSLTV 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-RPGGRLITLPGPDDVPADVPGHVRAVWML--VEPDHL-------GLREIA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RAVVVEQNGGPEVLVEREVARPEPGLNEVLVRVHAAGVNPVDPKTRA----SGALIEWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKYPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 KAVIIE---GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 15; Length 308;
6.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Obligation, Kari L.
APPLICANT: Construction, Mari L.
APPLICANT: Apallicant wall, baniel
APPLICANT: Traniel, Judith W.
APPLICANT: Traniel, John D.
APPLICANT: Traniel, John D.
APPLICANT: Tanmonto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamonto, Robert T.
APPLICANT: Vanamonto, Robert T.
APPLICANT: Vanamonto, Robert T.
APPLICANT: Vanamonto, Robert T.
APPLICANT: Vanamonto, Robert T.
APPLICANT: Vanamonto, Robert T.
APPLICANT: Vanamonto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: ELITRA-011A
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.8%; Score 207; DB 15; Length 30 Best Local Similarity 26.9%; Pred. No. 6.2e-11; Matches 98; Conservative 43; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RPEDAVGDVD-----VVLDGLGG-----
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: JP 2001-204089;
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-02;
ROWBER OF SEQ ID NOS: 15109
LENGTH: 308
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Patent No. US20020061569A1
GENERAL INFORMATION:
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R FILING DATE: 2000-05-23
R APPLICATION NUMBER: 60/207,727
RR FILING DATE: 2000-05-26
RR APPLICATION NUMBER: 60/242,578
RR APPLICATION NUMBER: 60/242,578
RR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Streptomyces avermitilis
US-10-156-761-8739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 ALTE 354
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168 QH-----THPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 ADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKM----EW-----HPS---TP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 GGPEVLRYDEVPIPEPGGPGEVLVRVHAVGVNPPDWYLRDGLTNLPPETRPKFSLPVIPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 GDKAVVKTD-VSVPELKEGTALVKVEAVAGNPTDW-----KHIAYKIGPEGS---ILGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%; Score 197; DB 15;
28.5%; Pred. No. 6.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 DYHDAGVIEQIKSKYPNLQH----VIDAVGSEDS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 DY-----TKSRPEELVHDVDLVLDAVGGPDS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29; Mismatches
                                                                                                                                                       APPLICANT: IKEDD, HARUO
APPLICANT: SHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIRB, TADAYOSHI
APPLICANT: SHIRB, TADAYOSHI
APPLICANT: HATTORI, WASHIRA
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: 3002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHRA, TADAYOSHI
APPLICANT: HATYORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PLILNG DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-214089
                                                                Sequence 8218, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9593, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.59
Warches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-156-761-8218
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Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERIES
FILE REPRENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
56 PEGSILGCDIAGTVVKLGPNASTDLKVGDTGFG-----FVHGASQTDPKNGAFAEYARVY 110
                                        61 EPPFVLGWDVSGVVEATGIGVAR-FKPGDEVFGMLSYPFGH-----GSHAEYVTAP 110
                                                                                                                                                                                                            111 PPLFYKSNLTH--STADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQ 168
                                                                                                                                      111 ARAF----AHKPSGVDHIQAG-----ALPLVSLTAWQAL-----VETADVRPG 149
                                                                                                                                                                                 169 HTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVI 228
                                                                                                                                                                                                                                                                            229 EQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKI 288
                                                                                                                                                                                                                                                                                                         115 YK-SNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SIPEAYKVTADSLP----ATLLEVVPM 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY----ARVYPPLF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 HKPNNLT-----PG----QNV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 LIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHE-KLLKSYGADDVFDYHDAGVIEQIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KHTNGNGFEVIFDTVGGKNLDHSFEAAVNGTVITIAARSTHDLSPLHAKGLSLHVTFM 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIESIPEEIRKD--NVKIDITLLYRASGQEILLGATRF----PASPEYHEATVKFVKFI 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 TQKAVIIE--GDKAVVKTD-VSVPELKEGTALVKVEAVAGNPTDWK---HIAYKIGPE-G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TMKAQIIHSFGDSSVFQLEKVSKPKLLPGHVLIDVKATSVNPIDTKMRSGAVSAVAPEFP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%; Score 197.5; DB 12; Length 28.1%; Pred. No. 5.4e-10; tive 51; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKYPN---LQHVIDAVGSED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                ::| ||
259 -LRMLVDAS 266
                                                                                                                                                                                                                                                                                                                                                                     289 DITLLYRAS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-369-493-16579
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11505
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                                                                                                                           163 AQIKPYS-----RVFIWAGSSGVGVAGIQLAKAFNAFV-ITTAGNBEKAKKCKELGADLV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKGKYPNLQHVIDAVGSED 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DTGFGFVHGASQTD----PKNG 101
                                                                                              102 AFABYARVYPPLFYKSNLTHSTADEISEGPVKN--PESAASLPVSLTTAGVSLCHHLGSK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 PNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 NFESAASLPVSLTTAGVSLCH----HLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 SMEQAASIPLVGLTAWQALIEVGKVKSGQK------VPIQAGSGGVGTFAIQL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 SI-------PEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                  62 LGSDVSGVVEKVG-SLVKAVKEGEEVIIAPGLSCGVCWDCQSGRDNHCKDYDILGLKNKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 DMPNPVIGANDVLVRIHATAINLLDSKVRDGEFKLFLPYR---PPFILGHDLAGTVIRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 ANV-ROPKTGDEVF----ARPROHRVGTFAEMIAV-------DAADLALKPTSL
                                                                                                                                                                                           160 MEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 DVSVPELKEGTALVKVEAVAGNPTDWK-----HIAYKIGPEGSILGCDIAGTVVKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 328;
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9.7%; Score 186.5; DB 12;
Best Local Similarity 27.6%; Pred. No. 5.8e-09;
Matches 85; Conservative 38; Mismatches 118;
                                                                                                                                                                                                                                                                                     220 FDYHDAGVIEQIKSKY-PNLQHVIDAVG 246
                                                                                                                                                                                                                                                                                                               217 FNHYKDDVVKKVREVFKEGVDVVVDHIG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11505, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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; Sequence 12902, Application US/10369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11505
       61 LGCDIAGTVVKLGPNASTDLKVG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 MRAEGOOL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 -RASGQEI 301
                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-369-493-11505
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Publication No. US20030233675A1

SEREMAL INFORMATION:

APPLICANT: Cao, Yongwel

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)8

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

WUMBER OF SEQ ID NOS: 47374

SEQ ID NO 102

LENGH: 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 IESIPEEIRKONVKIDIT---LLYRASGQEILLGATRFPASPEYHEATVKFVKFINPHLN 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : | ::
---RELTPLID 295
                                                                                                                                                                                                                                                                                                                                                                            57 EGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 SNLTHSTADEISEGPVK-NPESAASLPVSLTTAGVSLCHHL----GSKMEWHPSTPQHTH 171
                                                                                                                                                                                                                                                                                                               2 KTFMIERYGDKAGVRAGEMPDPQVGADDILVQIHAASVNPLDLRLRDGDFKAFLPYRL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 PLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 KAVIIEG----DKAVVKTDVSVPELKEGTALVKVEAVAGNPTD-WKHI-AYKIGPE-GSI
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QDDVAAKPATLTMEBASLPLVALTSWQALVERARVMPGQK-----
                                                                                                                                                                                                                                      66; Mismatches 135; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                           Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 193; DB 12; Length 343; larity 28.7%; Pred. No. 1.5e-09; Conservative 43; Mismatches 94; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 NGDIHHMNIKVFSNGLDDVPALTEGIKEGKNKNVKYVARL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : :|| : :|| : :|| 296 TGKIRPVVDRVFP--FAETRQAMEYVEKGRAKAGKVVVAM 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : :: | : :: | : :: | : :: | SALSFRTRRRAKRRNVTYSFLFMKASGDQL--------
                                                                                                                                                                                           DB 15;
                                                                                                                                                                                        Score 193.5; DB 1
Pred. No. 1.3e-09;
                                                                                            ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9593
                                                                                                                                                                                        10.1%;
23.5%;
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9593
LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Aquifex aeolicus
US-10-369-493-102
                                                                                                                                                                                                                                      94; Conservative
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 77; Conserv
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US-10-369-493-102
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Best Local S
Matches 77
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APPLICANT: Cao, Yongwei
APPLICANT: Ainkle, Gregory J.
APPLICANT: Slater, Seven C.
APPLICANT: Slater, Seven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPRENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                        115 YKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCH----HLGSKMEWHPSTPQHT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 GPEGSILGCDIAGTVVXLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFABYARVYPPLFYKSNL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 THSTADRISECPVKN--FESAASLPVSLTTAGVSL--CHHLGSKMEWHPSTPQHTHPLLI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 WGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 PNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEBIRKDNVKIDITLLYR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 KNYDAVFDTIGG-TTLEKSFNIIKSG--GNIVSVSGMPNARFGKEFGSGFFK---TLLFS 201
                                                                                                                                                                                                                 -----HIAYKI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 VLSGYDLVLNSQDAKTLEKSLNVLRPGGKLISISGPPDVAPARSLKLESAPAFCRQN 259
                                                                                                                                                                                                                                              2 KAFVV---DKYKKKGPLRLADMPNPVIGANDVLVRIHATAINLLDSKVRDGEFKLFLPYR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ILGNDFSGVIVKVGSQV-TRFKVGDAIY-----ARPRKNKIGTFAEYIAIH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 IKSKYPNLQHVIDAVGSEDS---IPEAYKVTADSLPATLLEVVPMTIESIPEEIRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                    Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 276;
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                                                                                                                                                                   Indels
                                                                                                                                                                                                                 8 KAVIIEGDKAVVK-----TDVSVPELKEGTALVKVEAVAGNPTDWK-
                                                                                                                  DB 12;
                                                                                                                  9.5%; Score 181.5; DB 12; 28.3%; Pred. No. 1.8e-08; tive 37; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16435, Application US/10369493
Publication No. US20030233675A1
                                    ; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Bacillus thuringiensis
US-10-369-493-16435
                                                                                                                                          Best Local Similarity 28.3
Matches 84; Conservative
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LENGTH: 333
                          TYPE: PRT
ORGANISM:
                                                                                                                       Query Match
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                                      APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Godman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12902
LENGTH: 353
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Coldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8 II MINGRER: US/10/369,493
CURRENT PAPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 IPFTGGRTLICGLPASPGLDFAGKIVSVHPKNRTEFBPGQ----LVYGCLARPRTFGTTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 PSTPOHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNVKIDITLLYRASGQEILLGATRFPASPEYHEATVKFVKFINPHLNNGDIHHMNIKVFS 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 YKIGPEGSIL-----GCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYARVYPPLFYKSNLTHSTADE1SEGPVKNFESAASLPVSLTTAGVSLCHHLG-SKMEWH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 DAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GSILTAFWRAITPRFLGGGRRWFVPLMMA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSGPR----VFINGGSGGCGVFAIQIAKMLGC--QVTTTCSGRNIELVRDLGADEIIDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VPTTOKAVIIEGDKAVVKTDVSV-----PELKE--GTALVKVEAVAGNPTDWK---HIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.5%; Score 182; DB 12; Length 353; Best Local Similarity 23.6%; Pred. No. 1.7e-08; Matches 90; Conservative 57; Mismatches 149; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-369-493-14785
; Sequence 14785, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSKEDLVEVGNLLKEGKLRTVK 323
                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-12902
  No. US20030233675A1
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60 ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNL 119
                                                                                                                                                                                                                              120 THSTADEISEGPVKNPESAASLPVSLTTAGVSLCHHL-----GSKMEWHPSTPQHTHPL 173
                                                                                                                                                                                                                                                      174 LIWGGATAVGQQLIQVAKHINAYTKIVTVAS-KKHEKLLKSYGADDVPDYHDAGVIEQIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 ILGFDAAGEVVAVGSQV-TLFNVGDK--VFYAGSNQ----RPGSNAEY------ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 THSTADE--ISEGPVK-NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 -- OVVDERLVGHAPOSLGAHDAAALPLVALTAWESLFDRIG-----VTOSTTGTLLVL 163
                                                                                                 6 KAVDIRGGKGERDALPINPQTPKPSPTEGQALVRVKAPGINRMDIVQRRGFYPLPPQAPA 65
                                                                           8 KAVIIEG-----DKAVVKTDVSVPELKEGTALVKVEAVAGNPTD--WKHIAYKIGPEG-S 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 SIPSDÓPDFLID-----VEVDRPTPGPHDLLVHIEAVSINPVDTK-VRMRAGKQKHPK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVBAVAGNPTDWKHIAYKIGPE--GS
 Length 335;
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9.2%; Score 177; DB 12;
17.2%; Pred. No. 4.7e-08;
.ve 33; Mismatches 102;
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ilarity 29.4%; Pred. No. 3.4e-07;
Conservative 31; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REPRENCE: 249-125 US/09/738,626 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 99/317484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 6825
LENGTH: 337
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6825
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211 KHTDGNGVDYIVDFVGA 227
                                                                                                                                                                                                                                                                                                                                                                                   233 SKYP--NLQHVIDAVGS 247
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                 ilarity 27.2%;
Conservative 3
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HAYASHI, MIKIRO
CCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIKO
IKEDA, MASATO
OZAKI, AKIO
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Best Local Similarity
....hes 69; Conservat
                   Best Local Similarity
Matches 70; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
   Query Match
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                   ----HLNNGDIHHMNIKVFSNG 345
                                           TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
                 ASGQEILLGATRFPASPEYHEATVKFVKFINP
                                                                                         346 LDDVPALTEGIKEGKNKNVKYVARL 370
                                                                                                                   :| :|:| | :|:
252 FEDAQKAMEYSESGRAKG-KIIAKI 275
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Publication No. US20030233670A1
GENERAL INFORMATION:
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Padmavathi, Manchikanti
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Deikman, Jill
Deng, Molian
Dong, Jinzhuo
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Malloy, Kathleen A.
McKiel, Christine L.
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APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ball, James A.
APPLICANT: Ball, James A.
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Laccetti, Lucille B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson, G. Richard
Jung, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salligan, Meghan M.
Hinchey, Brenda S.
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Lund, Adrian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephen M.
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Start, William G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chao-Qiang
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eng, Xiaoping
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Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang, Qiang
Zhao, Yajuan
Zhou, Li
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SEQ ID NO 679
LENGTH: 335
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; ORGANISM: Zea maye
US-10-310-154-679
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GENERAL INFORMATION:
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GEORY J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
PRIOR PILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 RVVKT-TNIVDNFRVGEIVFG-----RQAPTQHGACGQY-----IVASANACASLPSGV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 SEGPVKNFESAASLPVSLTTAGVSLCHHL--GSKMEWHPSTPQHTHPLLIWGGATAVGQQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VFLNGGSGGVGSF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 GIQIAKALGCHVTVSCSAAKAEQ--CKALGADDIIDYTAVDVCQALKERGGVFKLSVDNV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ----ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 NLPYVPGKDGAGFVELVGESVK-NVKVGDR----VWYGSEAD----STAEYVAVNRPF-- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 KSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GDVILV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TVVYLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEI 127
                                                                                                                                                                                                                                                                                                                                            18 VVKTDVSVPELK----EGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL-----GCDIAG
                                                                                                                                                                                                                                                                                                                                                                             186 LIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S SSWRAAVVRRFGAPDVIEAVESDMPRLEKNOVLVRNYAAGVNPVD---TYIRAGQYGKIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TTQXAVIIE--GDKAVVK-TDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGS--
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                                                                                                                                                                                                                                       Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
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                                                                                                                                                                                                                                     8.3%; Score 160; DB 12;
25.6%; Pred. No. 1.9e-06;
tive 45; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 -----DVDEAASLPCAGLTAYQTIAPNVKPGDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-369-493-5302
; Sequence 5302, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 G----LPAELYKAGDDYL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Caenorhabditis elegans
PRIOR APPLICATION NUMBER: US
                                                                                                                                                        ORGANISM: Neurospora crassa
                     PRIOR FILING DATE: 2002-02-
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3394
LENGTH: 333
                                                                                                                                                                                                                                                             Best Local Similarity 25.6
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5302
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Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-369-493-5302
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; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Glater, Steven C.
; APPLICANT: Gladman, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Gladman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TILE REFERENCE: 38-10 (52052)8
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT PILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 VVBETGEGV-TGFAVGDEVFG------NPVAGGYAQYA-VLP-----VTTTAHKPAG-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LSFTDAATLPVAAATA-----YDGVRQLGLPSGA----TLLITGAGGGVGVAAV 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEG-----SILGCDIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                           231
                                                         GGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 163; DB 15; Length 306;
28.3%; Pred. No. 8.5e-07;
tive 35; Mismatches 94; Indels 4
                                                                                                                                                                                                                                                                                                      APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
ITLE OF INVERTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
                                                                                                                                                                                                       Sequence 8836, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptomyces avermitilis US-10-156-761-8836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 28.38 Matches 69; Conservative
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ORGANISM:
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Sequence 14009, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Gao, Yongwei

APPLICANT: Gao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Wanteny S.

APPLICANT: Goldman, Warnfeny Barry S.

APPLICANT: Goldman, Wanteny S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION NUMBER: US/10/369, 493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 PKTYSRDYSGVIIKAGKDVDNRWKVGDKVNGMYSHIYG-----BRGTLTHYLILNPAKD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 - PLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 VK-NPESAASLPVSLTTAGVSLCHHLGSKMEW----HPSTPQHTHPLLIWGGATAVGQOL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GSILGCDIAGTVVKLGPNASTDLKVGDTGFGF---VHGASQTDPKNGAFAEYARVYP--- 111
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                                                                                                                                                                                                                                                                                                                                                                                     6 TOKAVIIEGDKAVVKTDVSVPELK----EGTALVKVEAVAGNPTDW-KH---IAYKIGPE
                                                                                                                                                                                                                                                                                                                                                                                                                  7 TNKSVTYVNNTTPVTITSSELDLRSCYQDDEVVIEVHAAALNPIDFITHQLCNSYIFGKY
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                                                                                                                                                                                                                                                                                                                                  Indela
                                                                                                                                                                                                                                                                               Query Match

8.0%; Score 154; DB 12;
Best Local Similarity 23.5%; Pred. No. 6.3e-06;
Matches 63; Conservative 49; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 IKS-KYPNLQH-----VIDAVGSEDSIP 252
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1893
LUGTH: 316
                                                                                                                                                                                                    ORGANISM: Saccharomyces cerevisiae US-10-369-493-1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-369-493-14009
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Publication No. US20030233675A1
GENERAL INFORMATION
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
                                                                             WGGATAVGQQLIQVA --KHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKS 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 IPTKWKAWVYREHGNVADVLGLDPELKVPELQEGQVLVKVLAAALNPVDAARMKGVIKLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 G----SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Expression FILE OF INVENTION: Modification of Gene Expression FILE OF INVENTION: MOMBER: US/10/137,036

CURRENT APPLICATION NUMBER: US-04-30

PRIOR FILING DATE: 2000-16-20

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-03-25

NUMBER OF SEQ ID NOS: 143

SOSTWARE FARESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8.1%; Score 155; DB 15;
Best Local Similarity 37.9%; Pred. No. 1.1e-06;
Matches 44; Conservative 16; Mismatches 42;
                                                                                                                                                                                                                                                                                                                            Sequence 65, Application US/10137036; Publication No. US20030101478A1; GENERAL INFORMATION:
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ORGANISM: Eucalyptus grandis
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APPLICANT: Rice, Stephen
APPLICANT: Eagleton, Clare
APPLICANT: Lasham, Annette
APPLICANT: Wood, Marion
                                                                                                                                                234 KYP-NLQHVID 243
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US-10-369-493-1893
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Qy 332 GDIHHMNIKVFSNGLDD 348	RESULT 28 US-09-738-626-3730 ; Sequence 3730, Application US/09738626 ; Publication No. US20020197605A1 ; GENERAL INFORMATION: ; APPLICANT: NAKAGAWA, SATOSHI ; APPLICANT: MIZGUCHI, HIROSHI ; APPLICANT: ANDO, SEIKO	ANT: HAYASHI, MIKIRO ANT: CCHIAI, KEIKO ANT: O'COLI HARUHIKO ANT: TYEISHI, NAOKO ANT: TYEISHI, NAOKO ANT: IKEDA, MASATO ANT: IKEDA, MASATO ANT: IKEDA, MASATO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO ANT: O'ZAKI, AKIO APPLICATION NUMBER: JP 00/189162 APPLICATION NUMBER: JP 00/189162 APPLICATION NUMBER: JP 00/280988 FILING DATE: 2000-08-03 OF SEQ ID NOS: 7059 APPLICATION VINDER: JO O'Z80988 APPLICATION NUMBER: JP 00/280988 APP	T, Conservative 33; Mismatch KAVVKTDVSVPELKEGTALV
Db 100 ANTDMAQAASLPLVALTAWQVLVETARLQKGQKVLIHAGSGGVGTVA 146 Qy 187 IQVAKHINAYTKIVTVASKKHBKLLKSYGADDVPDYHDAGVIEQIKSKYPN 237	Qy         238 LQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPWTIESIP 278           Db         195VLN8LGA-DVLEKSLKVLKPGGQLISISGPPTVQFAREHGLSWPLQQVMRLLSLGIR 250           Qy         279 EEIRKDNVKIDITLLYRASGQEI 301           E	RESULT 27 US-10-156-761-9450 is equence 9450, Application US/10156761 js Publication No. US20030119018A1 js Publication No. US20030119018A1 js APPLICANT: OWURA, SATOSHI ja APPLICANT: ISHIKAMA, UNN ja APPLICANT: SHIBA, HARUO ja APPLICANT: SHIBA, TADAYOSHI ja APPLICANT: SHIBA, TADAYOSHI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja APPLICANT: SARAKI, VOSHIYUKI ja PRIOR FILING DATE: 2001-05-30 ja PRIOR PILING DATE: 2001-05-30 ja PRIOR PILING DATE: 2001-08-02 ja PRIOR PILING DATE: 2001-08-02 ja PRIOR PILING DATE: 2001-08-02 ja PRIOR FILING DATE: 2001-08-02 ja PRIOR FILING SATE: 2001-08-02	Query Match         7.8%; Score 150; DB 15; Length 445;           Best Local Similarity 21.3%; Pred. No. 2.6e-05;         1 Accal Similarity 21.3%; Pred. No. 2.6e-05;           Matches 93; Conservative 52; Mismatches 142; Indels 150; Gaps 17;         1 MSVPTTOKAVILEGD

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CURRENT APPLICATION NUMBER: US/09/908,744
CURRENT FILING DATE: 2001.07.20
PRIOR APPLICATION NUMBER: PCT/FI01/00051
PRIOR FILING DATE: 2001.01.22
PRIOR PILING DATE: 2000.01.21
PRIOR FILING DATE: 2000.01.21
PRIOR FILING DATE: 2000.01.21
PRIOR PLING DATE: US 09/499,585
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                                                                                                                                                                                                                                                                                                                                                Query Match

7.7%; Score 148.5; DB 15; Length
Best Local Similarity 26.5%; Pred. No. 2.2e-05;
Matches 69; Conservative 37; Mismatches 99; Indels
          APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
SEQ ID NO 11902
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APPLICATION NUMBER: US 08/790,585
FILING DATE: 1997-01-29
APPLICATION NUMBER: US 08/368,395
FILING DATE: 1999-01-03

    TYPE: PRT
    CRGANISM: Streptomyces avermitilis
US-10-156-761-11902

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Plazanet-Menut Claire
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SHIBA, TADAYOSHI
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Gros H+kan
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Richard Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 VKVGDRVTSETTF-YVCGECDYCKEKQYNLCPHRKGIGTQQNGSMANY-----VLAREE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 GPGPIGLYLLQIAKEIGAFVIMTGITKDAHRLALAKKLGADVIVDTMKEDLAKVVNEITD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 LKVGD-----TGFGFV------HGASQTDPKNGAFAEYARVYPPLFYKSN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 LTHSTADEISEGPVKNFESAA-SLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 GATAVGQQLIQVAKHINAYTKIVTVASKKHE-KLLKSYGADDVFDYHD---AGVIEQIKS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 KYPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLL 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 352;
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7.5%; Score 144.5; DB 11; Length
Best Local Similarity 24.4%; Pred. No. 5.9e-05;
Matches 76; Conservative 35; Mismatches 109; Indels
PRIOR APPLICATION NUMBER: US 08/110,672
PRIOR FILING DATE: 1993-08-24
PRIOR APPLICATION NUMBER: US 07/973,325
PRIOR FILING DATE: 1992-11-05
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 69
LENGTH: 352
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Job time : 75 secs
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                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-09-908-744-69
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Title: Perfect score:

Sequence:

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

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   S. cerevisiae BAX-
C. albicans BAX-as
Human ORFX protein
A. terreus LovC de
Auxin-induced prom
Bucalyptus grandis
Enterococcus faeca
Listeria monocytog
Arabidopsis thalia
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| SIDSIJgcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSIJgcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSIJgcgdata/geneseqg-embl/AA1981.DAT:*
| SIDSIJgcgdata/geneseqg/emeseqg-embl/AA1981.DAT:*
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| SIDSIJgcgdata/geneseqg/genes
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                                                                                                                                                                                  US-10-081-644-2
1920
1 MSVPTTQKAVIIEGDKAVVK......ALTEGIKEGKNKOVVKYVARL
                 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 90 summaries
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ABG93300
ABP10927
AAY96748
AAB27051
AAU35110
ABB47714
AAG43467
                                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Novel human secret
          Arabidopsis thalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases
                                                                                                                                                                                                      cerevisiae BAX-associated protein fragment SEQ ID 332
                                                                                                                                                                                                                                                                                                                                                                                                           Luyten WHML, Reekmans RJ;
                                                                                               ALIGNMENTS
         AAG04620
AAG04619
ABB66217
ABB70568
ABP30052
AAY96753
 AAU30322
                                                                                                                                             ABG93187 standard; Protein; 376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 36; Figure 1; 344pp; English.
 2222222
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09-JAN-2001; 2001EP-0870003.
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                                                                                                                                                                                                                                                                                                                                                  22-DEC-2000; 2000EP-0870318
                                                                                                                                                                                                                                                                                                                               21-DEC-2001; 2001WO-EP15398
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                        (JANC ) JANSSEN PHARM NV
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                                                                                                                                                                                                                                                                                          WO200264766-A2
                                                                                                                                                                                  21-NOV-2002
                                                                                                                                                                                                                                                                                                             22-AUG-2002,
 128
128
128
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127.5
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                                                                                                                                                                ABG93187;
                                                                                                                          RESULT 1
                                                                                                                                    ABG93187
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887
887
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124 FRLCGXDKLPEGPVKSLEGAVSLPTAGMILIHSFGLDMTWKPSKAQRDQPILFWGG

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244 PYLVDCVSNTETIQQVYKCAADDLDATVVQLTVLTEKDIKEEDRRQNVSIEGTLLYLIGG

239 QHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASG

183

298 303

2 SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL 4 SIPETWKAVVIENGKAVVKQDIPIPELEEGFVLIKTVAVAGNPTDWKHIDFKIGPQGALL

59; Mismatches 109; Indels

Matches 201; Conservative

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Local Similarity

Query Match

55.5%; Score 1065.5; DB 54.0%; Pred. No. 1.4e-88;

described in the disclosure of the invention

376 AA;

Sequence

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63

Gaps ۳ ښ

DB 23; Length 376;

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Bax, Bax-resistance, cytostatic; fungicide; immunosuppressive; virucide; Vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal
                                                                                                      C. albicans BAX-associated protein fragment SEQ ID 558.
                                                                                                                                                                                                                                                                                                                                                                                           Reekmans
                                                                                                                                                                                                                                                                                                                                                                                           Luyten WHML,
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                         ABG93300 standard; Protein; 361
                                                                                                                                                                                                                                                                                                                                                                                         Contreras RH, Eberhardt I,
                                                                                                                                                                                                                                                                                                          22-DEC-2000; 2000EP-0870318.
04-JAN-2001; 2001EP-0870002.
09-JAN-2001; 2001EP-0870003.
                                                                                                                                                                                                                                                                                  21-DEC-2001; 2001WO-EP15398
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                              (JANC ) JANSSEN PHARM NV
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N-PSDB; ABQ76566.
                                                                                                                                                                                                  Candida albicans.
                                                                                                                                                                                                                             WO200264766-A2.
                                                                             21-NOV-2002
                                                                                                                                                                                                                                                        22-AUG-2002
                                                   ABG93300;
RESULT 2
            ABG93300
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synthetic

This invention describes a novel nucleic acid representing a

Bax gene. The Bax gene of the invention is useful for identifying Bax resistant yeast or fungi, identifying, or obtaining and identifying Bax-resistant yeast or fungi, identifying, or obtaining and identifying Candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the cinchipitor sequences of Bax-induced cell death. The products of the cinchipitor activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions, antibense molecules and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alleviating diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or preparing a medicament for modifying the endogenic flora of humans and preparing a medicament for modifying the endogenic flora of humans and cother mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease. Inschaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polypeptide associated with the Bax gene

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This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying candida spp. Sequences that are differentially expressed in a pathway eventually leading to programmed cell death. The products of the invention have cycostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cycostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cycostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cycostatic, fungicide; immunosuppressive, virucide and properties and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alleviating and cancer, or for preventing apported in certain diseases. The compounds or preparing a medicament for modified organism are useful for preventing and content mammals. The vaccine is useful for immunising against yeast or funging infections. Apported is useful for immunising against yeast or funging infections. Appropriate infections. Appropriate infections and diseases include autoimmune disease, funding and infections. Appropriate infections and propriate infections and propriate infections and propriate infections. Appropriate infections and propriate infections. Appropriate infections and propriate infections and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYP--PLFYKSNLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSTADEISEGPVKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AVGQQLIQVAKHINAYT-KIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESI-PEEIRKDNVKIDITLLYRASG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEILLGATRPPASPEYHEATVKFVKFINPHLNNGDIHHMNIKVFSNGLDDVPALTEGIKE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polypeptide associated with the Bax gene described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 KAVIIEG-----DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILG
infections or proliferative disorders, or for preventing apoptosis in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.6%; Score 473; DB 23; Length 361; 34.1%; Pred. No. 1.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Mismatches 150; Indels
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                                                                                Claim 36; Figure 2; 344pp; English
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                            certain diseases
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Human, open reading frame, ORFX, gene therapy, cancer; cirrhosis, hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX where X is 1-11491 [see Table 1 cm the specification). ABN15762 to ABN12752 encode the human ORFX proteins given in ABP0010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a squances can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the squances can be used in gene therapy. ORFX sequences can be used in the creatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, nameorthage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disbetes mellitus, systemic lupus erythematosus, hypertenaion, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease, autoimmune disorders such as multiple sclerosis, rheumatoid disease and autoimmune inflammatory eye disease. ORFX proteins are also cuseful for treating burns, incisions, ulcers, for treating osteoporosis, conception on injury in various tissues and conditions resulting from the parents of the parent of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the printed of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the parents of the paren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyrodidsm; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PNVDAARFAIGDYIYGVIHGASVRFPSNGAFAEYSAISSETAYKPAREFRLCGKDKLPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
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49.2%; Pred. No. 2.5e-20;
tive 16; Mismatches 47
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                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000; 2000US-206132P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-106308/14.
                                                                                                                                          myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABN26679
                                                                                                                                                                                                                                                 WO200192523-A2
                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                     06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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119 LTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPST---PQHTHP--L 173
                                                                                                                                                                                                                                                                                     ----PASPEYHEATVKFVKFINPHLNNGDIHHMNI 339
                                                                                                                                                                                                                                                                                                                  3 VPTTQKAVII--EGDKAVV---KTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to promoter sequences from eucalyptus and
                                                                                              174 LIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKS
                                                                                                                                                                                        234 -KYPNLQHVIDAVGSEDSIPBAYKVTADSLPATLLEVVPMTIESIPEE-IRKDNVKIDIT
                                                                                                                                                                                                                                       227 YIKNNLRYALDCITNVESTTFCFAAIGRAGGHY-----VSLNPFPEHAATRKMVTTDWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pine. The present protein is encoded by one such promoter. The coding sequence for the present protein is useful for modulating the transcription of DNA sequences of interest. The sequences may also be used to tag or identify an organism or its reproductive material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel promoter sequences useful for modulating transcription of plant
DNA sequences of interest and production of polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.9%; Score 266; DB 21; Length 318; 33.6%; Pred. No. 1e-15; tive 31; Mismatches 93; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoter; eucalyptus; pine; gene transcription.
                                                                                                                                                                                                                                                                                                                                                                                                         330 RVVQGGFDHIKQGMELVRKGELSGEKLVVRL 360
                                                                                                                                                                                                                                                                                                                                                                               340 KVFSNGLDDVPALTEGIKEGKNKNVKYVARL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Pages 64-65; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB27051 standard; Protein; 318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Auxin-induced promoter protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eagleton CK;
                                                                                                                                                                                                                                                                                     292 LLYRASGQEILLGATRF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2000; 2000WO-NZ00018
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99US-0146591
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les 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-647236/62.
N-PSDB; AAC62778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perera R, Rice SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200058474-A1.
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30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins shown in AAY96744-60 are encoded by 17 genes from a cluster in Aay967141 (ATCC 20542), which flank the NPKS cluster in Appergillus terreus (ATCC 20542), which flank the NPKS (nonaketide pollyketide synthase) gene is contained within the context of lovastatin production. The NPKS gene is contained within the context of the entire gene cluster but is not indicated here (see US5744350). The genes and proteins are named "ORF" or "Lov", where "Lov" signifies genes shown to be essential for lovastatin production. The portion of the gene cluster between ORF1 and the mid-region of LovF is referred to as the "DAB segment." Increasing lovastatin or monacolin J, production in a lovastatin-producing organism, comprises transforming the organism with a DAB segment, and expressing it (claimed). Lovastatin will also be transformation with the DAB segment and the entire LovF gene. The methods are used to increase biosynthetic production of lovastatin (with mat least 5-fold increase) which is an anti-hypercholesterolaemic agent, and also has some anti-fungal activity. Lovastatin inhibits the conversion of hydroxymmethylgluarylcoenzyme A (HMG-COA) into mevalonate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMG-COA reductase. The methods can also be used to increase production monacolin J (claimed), which has anti-fungal activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEY----ARVYPPLFYKSN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                        Lovastatin, D4B segment, monacolin J, dehydrogenase, LovC, anti-lipemic, HMG-COA reductase inhibitor, anti-hypercholesterolaemic, anti-fungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PTTQKAVII-EGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPOQTAL TVNDHDEVTVWNAAPCPMLPRDQVYVRVEAVAINPSDTK-MRGQFATPWAFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing lovastatin or monacolin J production in an organism, as antihypercholesterolemic or antifungal agents, comprises transforming the organism with a D4B segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.9%; Score 266.5; DB 21; 26.3%; Pred. No. 1.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 62-63; 116pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park C;
                                                                                                                       AAY96748 standard; Protein; 363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                            A. terreus LovC dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US29583
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                                                                                                                                                                                                                 (first entry)
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    122 KKLNGFSKII 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-442660/38.
                                                                                                                                                                                                                                                                                                                                                                            Aspergillus terreus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA51300
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                                                                                                                                                                  AAY96748;
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Best Local Similarity
 318 AA;
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  Sequence
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                                                     114 FYKSNLTHSTADEISEGPVK-NFESAASLPVSLTT-----AGVSLCHHLGSKMEWHPS 165
                                                                                                         166 TPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDA 225
G----SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPL 113
                                                                                                                                    ---HGKSLLVLGGAGGVGTLIIQLAKEVFGASRVAATSSTGKLELLKSLGADLAIDYTKV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide promoter sequences from Pine and Eucalyptus useful for modifying expression of endogenous and/or heterologous polynucleotides in transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                     Promoter; pine; leaf; root; flower; pollen; bud; meristem; xylogenesis; temporally regulated promoter; Pinus radiata; Eucalyptus grandis.
               67 GPSLPAVPGYDLAGVVVVKVGREVK-ELKVGDEVYGFMFHAK----KDGTLAEYAVEESF
                                                                      212 N-FEDLPEKF---DVVYDTVGEIERAAKAVK 238
                                                                                                                                                                GVIEQIKSKYPNLQHVIDAVGSEDSIPEAYK 256
                                                                                                                                                                                                                                                                                                                                             Bucalyptus grandis promoter polypeptide #4.
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FLETCHER CHALLENGE FORESTS IND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 80-81; 121pp; English.
                                                                                                                                                                                                                                                            AAU80748 standard; Protein; 318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-2001; 2001WO-NZ00115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2000; 2000US-0598401
28-NOV-2000; 2000US-0724624
                                                                                                                                                                                                                                                                                                                 (first entry)
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N-PSDB; ABK17043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice S,
                                                                                                                                                                                                                                                                                                                                                                                                                Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200198485-A1.
                                                                                                                                                                                                                                                                                                                 26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perera R,
                                                                                                                                     155
                                                                                                                                                                526
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113
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                                                                                                                                                                                                                                                                                                                                          114 FYKSNLTHSTADEISEGPVK-NFESAASLPVSLTT-----AGVSLCHHLGSKMEWHPS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 TPQHTHPLLIWGGATAVGQQLIQVAXHINAYTKIVTVASKKHBKLLKSYGADDVFDYHDA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 ---HGKSLLVLGGAGGVGTLIIQLAKEVFGASRVAATSSTGKLELLKSLGADLAIDYTKV 211
                                                                                                                                                                      99
                                                                                                                                                     3 VPTTQKAVII--EGDKAVV---KTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE
                                                                                                                                                                                                                           58 G----SILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFABYARVYPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential agenes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                               122 -----LALKPKKLRFGBASLPVVIQTAYGGLBRAGLS------
                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
  Length 318,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis cellular proliferation protein #397.
                                                          IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                          93;
DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Syskind JW, Wall D,
  Score 266; DB 2:
Pred. No. 1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 N-FEDLPEKF---DVVYDTVGEIERAAKAVK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 GVIEQIKSKYPNLQHVIDAVGSEDSIPEAYK 256
                                                          31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3, Seq ID No 10703, 511pp; English.
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23-MAY-2000, 2000US-206648P.
26-MAY-2000, 2000US-207727P.
23-OCT-2000, 2000US-242578P.
27-NOV-2000, 2000US-253825P.
22-DEC-2000, 2000US-253825P.
     13.9%;
33.6%;
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                                                          91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu HH;
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CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense mucleic acids can also be used to obtain antibodies capable of binding to the express these proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen Cf or homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an CG a wide variety of organisms. The present sequence represents an CG the printed specification, but was obtained in electronic of the printed specification, but was obtained in electronic C format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from WIPO at CG format directly from format directly from MIPO at CG format directly from MIPO at C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 FYKSNLTHSTADEISEGPVKOFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQI-- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---KSKY----PNLQHVIDAVGSEDSIPEAYK-VTADSLPATLLEVVPMT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; gene therapy, vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 265; DB 22; Length 3:30.4%; Pred. No. 1.3e-15; Indels ive 42; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes protein #418.
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Best Local Similarity
Matches 106; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                          322 AA;
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monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and EC for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication of sequence and proteins encoded by it are useful in pharmaceutical and esquence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. Comorcytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO CC at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHCASQTDPKNGAFAEYARVYPPLFYKSNL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .20 THSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 LAPLPEGIS------PDEAASIPLAGLTAWQALFDH--AKL------QKGEKVLIHAGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 TAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 VVFDTMGGQIE-TDSYDVLKEG-TGRLVSIV----GISNEDRAKEKNVTATGIMLQPNG 261
                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
       Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P Daniels J, Goobel W, Kreft J, Kuhn M, Ng E. Vazquez-Boland JA; Dominguez-Bernal G, Garido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Jolaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 KAVIIE---GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWK----HIAYKIGPE-GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KAVVIENYGGKEELKEKEVAMPKAGKNQVIVKBAATSINPIDWKLREGYLKQMMDWEFPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 ILGWDVAGVISEVGEGV-TDWKVGDEVF----ARPETTRFGTYAEYTAV-----DDHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 HVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLY-RASG
Glaser P, Kunst.,
No E, Vazquez-Boland JA;
Amend
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                                                                                                                                                                                                                                                                                                                                                                                                                to the genome sequence of Listeria
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     Nedjari H,
                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID No 419; 192pp; French.
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Les 102; Conservative
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                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
          Arabidopsis thaliana protein fragment SEQ ID NO: 54334.
                                                                                                                                                                   99US-0121825.
99US-0123180.
99US-0125788.
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                                                                            Arabidopsis thaliana.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 54335.
                                         AAG43468 standard; Protein; 309 AA
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990S-0126785.
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                                                                                                                                                                                                                                                                                                                                                                               Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 24972.
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113 L--PYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHT 170
                                                                                                         171 HPLLINGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQ 230
                                                                                                                    -GPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKN-GAFAEYARVYPP 112
                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 24973.
                                                                                                                                               231 IKSKYPNLQHVIDAVGSEDS----IPEAYKVTA 259
                                                                                                                                                                  287 LPDKY---DVVPDAIGMCDKAVKVIKEGGKVVA 316
                                                                                                                                                                                                                   AAG22153 standard; Protein; 309 AA
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99US-0125248.
99US-0126264.
99US-0126268.
99US-0126785.
99US-0128714.
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99US-013049.
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                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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29-MAR-1999;
01-APR-1999;
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16-APR-1999;
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990S-0147935

990S-0148171

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990S-01481841

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99US-0162142.
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Best Local Similarity 31.55
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25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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99US-0134941. 99US-0135124. 99US-0135353.

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99US-0135629. 99US-0136021. 99US-0136392. 99US-0137222. 99US-0137222. 99US-013722. 99US-013724. 99US-013724. 99US-0138440. 99US-0138119. 99US-0139119.	99US-0139492. 99US-0139454. 99US-0139455. 99US-0139456. 99US-0139456. 99US-0139460. 99US-0139461. 99US-0139461. 99US-0139461. 99US-0139461. 99US-0139463. 99US-0139463. 99US-0139817. 99US-013989. 99US-0140823. 99US-0140823. 99US-0140823. 99US-0141842. 99US-0141842. 99US-0141842. 99US-0142055.	99US-0142920 99US-0143542 99US-0144005 99US-0144005 99US-0144086 99US-0144325 99US-0144331 99US-0144331 99US-0144331 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0144332 99US-0145086 99US-0145086 99US-0145087 99US-0145192 99US-0145192 99US-0145192 99US-0145193 99US-0145145 99US-014518 99US-014518
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                                                                                                                                                                   QVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGS 247
                                                                                                 KLGPNASTDLKVGDTGFGFVHGASQTDPKN-GAFAEYARVYPPL--FYKSNLTHSTADEI 127
                                                                          DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKI----GPEGSILGCDIAGTVV
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                                                  Gapa
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                                  Length 309;
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                                                                                                                                                                                                                                                                                                              Enterococcus faecalis cellular proliferation protein #638.
                                                 99; Indels
                                                                                                                                                                                                                                                                                                                             Antisense, prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                Query Match
Best Local Similarity 32.0%; Pred. No. 5.4e-14;
Matches 82; Conservative 35; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Seq ID No 10944; 511pp; English.
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-20727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-25365SP.
22-DEC-2000; 2000US-25363P.
16-FSB-2001; 2001US-269319P.
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99US-0161992.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis
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28-OCT-1999;
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Yamamoto RT,
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genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded sureus, Salmonella typhi, Klebsiella predemoniae, Pseudomonas aeruginosa and Enterococus facealia. The promotion is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organism. The present sequence represents an essential prokaryotic cellular proliferation protein.

Conce: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LILGSDFAGIVVSVGKKVQ-NFRLGDAVYGRV-----PKNRVGTFAEYIAVDQAAVAM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 IWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SILGCDIAGTVVKLGPNASIDLKVGDTGFGFVHGASQTDPKN--GAFABYARV--YPPLF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 YKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 QKELAIE-----EVPLPTIHDNDVLVKIIAASINPIDLKTKDGKVKMLLNYQM---P 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 QKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKH-----IAYKIGPEG
their use in the discovery of novel antibiotics, the essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
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Matches 83; Conservative 39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       API; 2002-043418/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2807446-A1.
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drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida infection or cancer)
                        New protein-protein complexes of Saccharomyces cerevisiae, useful in
                                                                                                         The present invention relates to complexes between Saccharomyces
                                                                                 Claim 6; Page 41; 357pp; English.
N-PSDB; ABT11258.
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 16
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                                                                                                                                                                                                                                                                                                                                       111 NLTK------EKAVAMPLTSLTAYELLFEKL-----EVTDKSKGKSLLIIN 150
                                                                                                                                                                                                                                                                                                                                                                                                                     GATAVGOOLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGV--IEQIKSKY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention is related to a Lactococcus lactis nucleotide acquence (ABA90521) and related proteins (ABB53300-ABB5521). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The protection of yourt and cheese.

Production of yourt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-07-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                        GCDIAGTVVKLGPNASTDLKVGDTGF--GFVHGASQTDPKNGAFAEYARVYPPL--FYKS 117
                                                                                                                                                                                                                                                                                                                                                                      NITHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast; protein-protein interaction; Selected Interacting Domain; SID (RTM); secretion yield; cancer; neurodegenerative disease; fungicide;
                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                       8 KAV-IIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGS----IL
                                                                                                                                                                                                                                                    Gaps
sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                           9.0%; Score 173; DB 23; Length 328; 28.8%; Pred. No. 3.3e-07; Live 43; Mismatches 91; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast selected interacting domain protein SEQ ID NO: 16.
                                  SEQ ID No 732; 2504pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ10941 standard; Protein; 421 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002; 2002WO-EP02299
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           lactis and related species
                                                                                                                                                                                                                                      Local Similarity 28.8 tes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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VDYILILNAV 219
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                                                                                                                                                                                                    328 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ10941;
                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
                                                                                                                                                                                                      Sequence
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cerevisiae Selected Interacting Domain (SID (RTM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that medulate the interaction of proteins, for developing yeast strains with better secretion yield of protein, and in gene therapy. The protein complexes, polypeptides and polynucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                               Length 421;
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                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                            8.9%; Score 171; DB 23;
46.5%; Pred. No. 7.3e-07;
iive 12; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C glutamicum protein fragment SEQ ID NO: 6825
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Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG93071 standard; Protein; 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.5'
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 KNKNVKYVARL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 KNSGEKLVAVL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coryneform bacterium; an organic acid synthesis.
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Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-376931/40.
                                                                                                                                                                                                                              421 AA;
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Tateishi N,
                                                                                                                                                                                                                                 Sequence
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Sequence
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31-AUG-1
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                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFABYARVYPPLFYKSNL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 THSTADE -- ISEGPUK-NFESAASLPVSLTTAGVSLCHHLGSKOMEWHPSTPQHTHPLLIW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 -- QVVDERLVGHAPQSLGAHDAAALPLVALTAWESLFDRLG------VTQSTTGTLLVL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 SIPSDQPDFLID-----VEVDRPTPGPHDLLVHIEAVSINPVDTK-VRMRAGKQRHPK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE--GS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleocide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitemin; cofactor; polyketide; elagmes; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 ILGFDAAGEVVAVGSQV-TLFNVGDK--VFYAGSNQ---RPGSNAEY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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                                                                                                                                                                                                                                                                                                                                                                                                         8.8%; Score 168; DB 22; Length 337;
29.4%; Pred. No. 9.9e-07;
tive 31; Mismatches 93; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB79594 standard; Protein; 337 AA
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9908-1031424.
9908-1031424.
9908-1031428.
9908-1031431.
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99DE-1031413
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Best Local Similarity 29.48
Marches 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                              337 AA;
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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08-JUL-1999
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metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and caidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleoside, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (C [III) encoded by them are used for diagnosing the presence or activity of corraining them are used to map genomes of organisms related to C corraining them are used to map genomes of organisms related to C containing them are used to map genomes of organisms related to C containing them are used to map genomes of organisms related to C containing them are used to map genomes of organisms related to C containing them are used to map genomes of organisms related to C containing them are used to map genomes of organisms related to C c glutamicum, identify and localise C glutamicum sequences of interest, c revolutionary studies, in determining SMP protein regions required for metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 SIPSDQPDFLID-----VEVDRPTPGPHDLLVHIEAVSINPVDTK-VRMRAGKQKHPK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
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29.4%; Pred. No. 9.9e-07;
ive 31; Mismatches 93; Indels 4.
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N-PSDB; AAF71711.
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01-JUL-1
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                     177 GGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQI 231
                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 33853.
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08-APR-1999;
16-APR-1999;
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23-APR-1999;
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-MAY-1999;
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31-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9-APR-1999
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04-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVPTTQKAVIIE--GDKAV--VKTDVSVPELKEGTALVKVEAVAGNPTDWK------ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.7%; Score 167; DB 21; Length 363; 26.1%; Pred. No. 1.4e-06; ive 47; Mismatches 91; Indels 6.
990S-0149368
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Best Local Similarity 26.1%;
Matches 72; Conservative
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Length 363;
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990S-01381817-
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990S-014408S-
990S-014433S-
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                                                                                                                                ---HIAYKIGPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAE 105
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                                                                                                                                                                                                                                                PSTPQHT--HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFD 221
                                             SVPTTQKAVIIE--GDKAV--VKTDVSVPELKEGTALVKVEAVAGNPTDWK------ 48
                                                                    Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
    Gaps
    99
72; Conservative 47; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 33852.
                                                                                                                                                                                                                                                                                                                                                                                                222 YHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKV 257
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990S-0123180.
990S-0123548.
990S-0125788.
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99US-0127462.
99US-0128234.
99US-0128714.
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99US-0134768
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23-MAR-1999;
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AAG28580
  Matches
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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99US-0123180.
99US-0123180.
99US-0125788.
99US-0126785.
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99US-012945.
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99US-0130871.
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990S-0161404.
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990S-0161406.
99US-0145951
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-AUG-1999;
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                                                                                                                                                                                                                                                                                                      98
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120 AA-----EAAALPVAGLTALQALTNPAGLKLD---GTGKKAN-ILVTAASGGVGHYAVQ 169
                                                                                                                                                                                                                                                   228 PPSVPEPNLSENGKVIDITPGPNAM---WTYAVKKITMSKKQLVPLLL--IP---KAENL 279
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                                                                                                                                             14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP----EGSILGCDIAGT
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99US-0147103 99US-0147416 99US-0147416 99US-0147935 99US-0148341 99US-0148349 99US-0149368 99US-0149723 99US-0149723 99US-0149723 99US-0149723 99US-0149723 99US-0149723 99US-0149723 99US-011080 99US-0151082 99US-0151082 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083 99US-0151083

99US - 0142920 99US - 0143542 99US - 0143624 99US - 0144005 99US - 0144013 99US - 0144332 99US - 0144332 99US - 0144332 99US - 0144332 99US - 0144332 99US - 0144332 99US - 0144332 99US - 0144332 99US - 0144332 99US - 0144632 99US - 014508 99US - 014508 99US - 014508 99US - 014508 99US - 014508 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913 99US - 0145913

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The invention relates to identifying target proteins (ABB90790-ABB94016) for harbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypoptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                          Claim 5; SEQ ID NO 2125; 261pp + Sequence Listing; English
                     active polypeptide SEQ ID NO 2125.
                                          Herbicidal; plant; agriculture; herbicide
                                                                                                                        28-AUG-2001; 2001WO-EP09892
                                                                                                                                           28-AUG-2001; 2001WO-EP09892.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                             useful as herbicides.
                                                            Arabidopsis thaliana
                                                                                                                                                                                  Weidler
                                                                                                                                                                                                       WPI; 2002-269010/31
                                                                                                                                                              (FARB ) BAYER AG
                                                                                WO200210210-A2.
                     Herbicidally
   31-MAY-2002
                                                                                                    07-FEB-2002
                                                                                                                                                                                  Tietjen K,
                                                                                                                                                                                                                                                          organisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGPVKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PNLQH----VIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNV 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGLEHVQVPVPTPKSNEVCLKLEATSLNPVDWKIQKGMIRPFLPRKFPCIPATDVAGE
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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----KAEDAWAKSIDGH 320
                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                  2e-06;
                                                                                                                                                                                                                                                                                                                                                                                     8.6%; Score 164.5;
23.4%; Pred. No. 2e-
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                                                                                                                                99US-0159330.
99US-0159331.
99US-0159637.
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99US-0160741.
99US-0160767.
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99US-0160770.
99US-0160814.
99US-0160815.
99US-0160980.
99US-0155659.
99US-0156458
99US-01557117
99US-0157753.
99US-0157865.
99US-0158029.
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99US-0159329.
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99US-0161404
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99US-0161361
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99US-0162142
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                                      05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
08-OCT-1999;
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13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
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25-OCT-1999;
26-OCT-1999;
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                                                                                                                                                                                 VVEVGSGVK-NPKAGDKVVAVLSHLG-----GGGLABFA-----VATEKLTVKRPQEVG
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LAKLANAH--VTATCGARNIEFVKSLGADEVLDYKTPEGAALKSPSGKKYDAVHCANGI
                                                                                                                                               GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP-----EGSILGCDIAGT
                                                                                                 Gaps
                                                                                               65;
                                              DB 23; Length 329,
                                              8.6%; Score 164.5; DB 23; Length
13.4%; Pred. No. 2e-06;
.ve 56; Mismatches 141; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG39981 standard; Protein; 354 AA
                                                                     23.4%;
                                      Query Match
Best Local Similarity 23.48
Matches 80; Conservative
329 AA;
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ABB92914 standard; Protein; 329

RESULT 24

ABB92914

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990'S - 0139463

990'S - 0139463

990'S - 0139750

990'S - 0139817

990'S - 0139817

990'S - 0140354

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99US-0139462
       18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
23-JUN-1999;
23-JUN-1999;
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28-JUN-1999;
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09-AUG-1999
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                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                           Arabidopsis thaliana protein fragment SEQ ID NO: 49545.
                                                                                                                                                                    990S-0121825.
990S-0123180.
990S-0123180.
990S-0125788.
990S-0126264.
990S-0127465.
990S-0127465.
990S-0129845.
990S-0132484.
990S-0132484.
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990S-0134418.
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990S-013444.
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990S-0138094.
990S-0138540.
990S-0139119.
990S-0139452.
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99US-0139454.
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99US-0139457.
99US-0139469.
99US-0139469.
                                                                                                                                                     2000EP-0301439
                          (first entry)
                                                                                                Arabidopsis thaliana
                                                                                                                  EP1033405-A2
                                                                                                                                                    25-FEB-2000;
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05-MAR-1999;
09-MAR-1999;
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         AAG39981;
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258 PPSVPEPNLSENGKVIDITPGPNAM---WTYAVKKITMSKKQLVPLLL--IP---KAENL 309
                     -----PNLQH----VIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNV 286
                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                    287 KIDITLLYRASGOBILLGATRFPASPEYHEATVKFVKFINPH 328
                                                                                                         EFMVNLVKEGKVKTVI--DSKHPLS----KAEDAWAKSIDGH 345
                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 1332.
                                                                                                                                                                                                        AAG05068 standard; Protein; 262 AA
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990S-0123180.
990S-0123248.
990S-0125788.
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990S-0126783.
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990S-0134218.
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99US-0138540
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16-APR-1999;
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21-APR-1999;
23-APR-1999;
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                                                                                                                                                                      RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 164.5; DB 21; Length 3
23.4%; Pred. No. 2.2e-06;
tive 56; Mismatches 141; Indels
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13-0CT-1999
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-OCT-1999;
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Best Local S:
Matches 63
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14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP----EGSILGCDIAGT

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Gaps

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05-AUG-1999;
         04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
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                                       10-JUN-1999
14-JUN-1999
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                                                                                                                                                                  8-JUN-1999
 72 VVQVGSGVK-NFKAGDKVVAVLSHLG-----GGGLAEFA-----VATEKLTVKRPQEVG 119
                                                      120 AA-----EAAALPVAGLTALQALTNPAGLKLD---GTGKKAN-ILVTAASGGVGHYAVQ 169
                                                                           189 VAKHINAYTKIVTVASKKHEKLLKSYGADDVFDY---HDAGVIEQIKSKYPNLQHVIDAV 245
                                                                                     69 VVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEIS 128
                                             129 EGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQ 188
12 GAAGLEHVQVPVPTPKSNEVCLKLEATSLNPVDWKIQKGMIRPFLPRKFPCIPATDVAGE 71
                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 1331.
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990S-0134218.
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990S-0134319.
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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05-MAR-1999;
09-MAR-1999;
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01-JUN-1999;
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08-APR-1999
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28-APR-1999
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04-MAY-1999
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69 VVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEIS 128
                                                                         129 EGPVKNFESAASLPVSLTTAGVSLCHHLGSKWEWHPSTPQHTHPLLIWGGATAVGQQLIQ 188
                                                                                                         125 AA-----EAAALPVAGLTALQALTNPAGLKLD---GTGKKAN-ILVTAASGGGGHYAVQ 174
                                                                                                                                              189 VAKHINAYTKIVTVASKKHEKLLKSYGADDVFDY---HDAGVIEQIKSKYPNLQHVIDAV 245
                                      17 GAAGLEHVQVPVPTPKSNEVCLKLEATSLNPVDWKIQKGMIRPFLPRKFPCIPATDVAGE 76
                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                           14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP----EGSILGCDIAGT
Best Local Similarity 26.2%; Pred. No. 2.5e-06;
Matches 63; Conservative 35; Mismatches 110; Indels 32; Gaps
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99US-0130891.
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99US-0135124.
99US-0135353.
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06-APR-1999;
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28-APR-1999;
30-APR-1999;
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175 HTQAASLPYVALTAW-SAINKVGGLNDKNCTGKR----VLILGASGGVGTFAIOVMKAWD 229
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                                                                                                                                                                                                         FESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHIN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine, cell proliferation; cell differentiation, growth factor, haematopoiesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and agequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising ancleotide of the invention, methods of producing the novel polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematopoieeis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; matestasis; cancer; tumour; haematopoietic disorder; proliferation; matestasis; cancer; tumour; haematopoietic disorder; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; oconary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                            195 AYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVG--SEDSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    numan proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human IL-2R-associated protein 43 homologue, SEQ ID NO:2206
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27-APR-2000; 2000US-0560875.
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N-PSDB; ABA09080.
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                                                                                                                                                                                                                                                                                                          VVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEIS 128
                                                                                                                                                                                                                                                                                                                                                         102 VVQVGSGVK-NFKAGDKVVAVLSHLG-----GGGLAEFA-----VATEKLTVKRPQEVG 149
                                                                                                                                                                                                                                                                                                                                                                                                          129 EGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 GAAGLEHVQVPVPTPKSNEVCLKLEATSLNPVDWKIQKGMIRPFLPRKFPCIPATDVAGE 101
                                                                                                                                                                                                         14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP-----EGSILGCDIAGT
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signal transduction.
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                                                                                                   Query Match 8.4%; Score 162; DB 21; Length 2 Best Local Similarity 26.2%; Pred. No. 2.8e-06; Matches 63; Conservative 35; Mismatches 110; Indels
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                          99US-0161993.
     99US-0161992
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28-OCT-1999;
28-OCT-1999;
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antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention and we handlogy to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may that arise arise is stem cell growth factor activity; the invention may differentiation activity; itsue growth activity; the member activity; the member activity; the member activities; hemostatic or chemokinetic activity; tisue growth activity; the member activities or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions e.g., by protein or gene therapy. Such conditions and conditions e.g., by protein or gene therapy. Such conditions are useful for preventing, treating or amelorate disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, proliferative retinopathy, atherosclerosis, coronary heart disease, promote cell scowth. For example, such polypeptides may be used to promote wound repair (or nucleic acids encoding then may be used to promote cell growth. For example, such polypeptides may be used to augment or temmune disease or accidental damage. The polypeptides and nucleotides may also be used to augment or resplace cells damaged by illnes, autoimmune disease or accidental damage. The polypeptides and in the disease or accidental damage. The polypeptides and in the disease or accidental damage. The polypeptides and in the disease or accidental damage. The polypeptides and in the disease or accidental damage. The polypeptides and in the disease or acciden
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413 AA; Sequence

135 FESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHIN 194 195 AYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVG--SEDSIP 252 247 AH--VTAVCSQDASELVRKLGADDVIDYKSGSVEBQLKSLKP-FDFILDNVGGSTETWAP 303 76 ASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK-N 134 151 VKY-FKPGDEVW-----AAVPPWKQGTLSEFVVV------SGNEVSHKPKSLT 191 34 LVKVEAVAGNPTDWK--------HIAYKIGPEGSI-LGCDIAGTVVKLGPN 75 DB 22; Length 413; 8.3%; Score 158.5; DB 22; Length 27.8%; Pred. No. 9.8e-06; ive 39; Mismatches 96; Indels 253 EAYKVTADSLPATLL 267 Local Similarity 27.8 tes 71; Conservative Query Match a a ઠે a ò ઠે 셤

Search completed: January 10, 2004, 10:04:54 Job time : 80 secs

304 DFLKKWSGATYVTLV 318

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Mon Jan 12 09:40:45 2004

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

January 10, 2004, 09:56:13; Search time 37 Seconds (without alignments) 961.687 Million cell updates/sec Run on:

Title: Perfect score:

US-10-081-644-2 1920 1 MSVPTTQKAVIIEGDKAVVK......ALTEGIKEGKNKNVKYVARL 370

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 90 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	hypothetical prote		hypothetical prote	œ	oxidoreductase hom	auxin-induced prot	quinone oxidoreduc	zinc-binding oxido	quinone oxidoreduc	probable alcohol d	quinone oxidoreduc	zinc-binding oxido	alcohol dehydrogen	alcohol dehydrogen	zinc-binding dehyd	quinone oxidoreduc	alginate lyase BH0	zinc-binding dehyd	probable oxidoredu	NADPH2:quinone red		e qui	O	quinone oxidoreduc	probable quinone o	zeta-crystallin /	hypothetical prote	~	zeta-crystallin /
SUMMARIES	ΙΩ		S59418	S19414	AE1151	AF1510	T10824	E86371 .	AF3199	C83695	C70418	G83766	AH3214	B90457	T18230	AG3182	E86714	B83742	AD2699	D97481	AH3289	T10203	F97459	A82309	AI2677	A70871	PN0448	AC1858	CYGPZ	A54932
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	Length	376	376	368	313	313	317	309	353	324	343	322	334	m	*	N	N	m	m	m	m	329	4	m	N	N	N	-	329	. 331
*	Query Match	55.5			13.8			13.2		10.8				9.5								8.6			8.4	8.4		8.3		8.3
	Score	1065.5	1021.5	1015.5	264	260	259	254	218	208	193	187.5	187	176	175.5	173.5	173	172.5	171.5	171.5	170.5	164.5	164.5	164	162	161.5	191	159.5	159	158.5
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## ALIGNMENTS

RESULT 1 855149 hypothetical protein YNL134c - yeast (Saccharomyces cerevisiae) N/Alternate names: hypothetical protein JTF376; hypothetical protein N1214; hypothetical S,Species: Saccharomyces cerevisiae C,Species: Os-Jul-1995 #sequence revision 01-Sep-1995 #text_change 19-Apr-2002 C;Accession: S55149; S59254; S63079

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62

182

297

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A;Residues: 1:376 <KIR>
A;Cross-references: EMBL:U22383; NID:g2264349; PIDN:AAB64723.1; PID:g717077; GSPDB:GN0001
A;Experimental source: strain S288C (AB972)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 ISYLVDCVANQDTLQQVYKCAADKQDATIVELKNLTEENVKKENRRQNVTIDIIRLYSIG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGCDIAGTVVKLGPNAS-TDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKS-- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 NLTHSTADEISEGPVKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWG 177
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C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 GATAVGQSLIQLANKLNGFTKIIVVASRKHEKLLKEYGADELFDYHDIDVVEQIKHKYNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 LQHVIDAVGSEDSIPBAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRAS
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R,Grivell, L.A.; de Haan, M.; Maat, M.J.
submitted to the Protein Sequence Database, March 1992
A,Reference number: S19412
A,Accession: S19414
                                                                                                                                                                                                                                                                                          53.2%; Score 1021.5; DB 2; ilarity 51.7%; Pred. No. 3.9e-69; Conservative 67; Mismatches 110;
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A; Map position: 3R
                                                                                                                                                                                                                    SGD:S0004452
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Best Local Similarity
Matches 193; Conserv
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A; Residues: 1-368 < GRI>
                                                                                                                                                                                    A; Gene: MIPS: YLR460c
                                                                    A; Molecule type: DNA
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R; Mallet, L.; Bussereau, F.; Jacquet, M.
aubmitted to the EMBL Data Library, November 1994
A; Description: A 43.5 kb fragment of the chromosome XIV.
A; Reference number: S53136
A; Accession: S55136
A; Accession: S55136
A; Molecule type: DNA
A; Residues: 1-376 cMAL>
A; CMALET, L.; Bussereau, F.; Jacquet, M.
R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; A; Cmallet, L.; Bussereau, F.; Jacquet, M.
A; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; R; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; R; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; R; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; R; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; R; Mallet, L.; Bussereau, F.; Jacquet, M.
A; Reference number: S63069
A; R; Molecule type: DNA
A; Reference number: S63069
A; R; Molecule type: DNA
A; Reference number: S63069
A; R; R; Molecule type: DNA
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A; Residues: L; Palsereau, F.; Jacquet, M.
A; Residues: S63079
A; Molecule type: DNA
A; Residues: S63079
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A; Residues: S63079
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A; Residues: S63079
A; Map position: 14L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNL 238
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hypotherical protein YLR460c - yeast (Saccharomyces cerevisiae)
hypotherical protein MyDotherical protein L9122.7

NyAlternate names: hypothetical protein L9122.7

C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change
C;Accession: S59418

R;Kirsten, J

Submitted to the EMBL Data Library, March 1995

A;Description: The sequence of S; cerevisiae cosmid 9122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 GKNKNVKYVARL 370
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C.Species: Listeria innocua [imported] - inscenta innocua [strain Cippii262]
C.Species: Listeria innocua [revision 27-Nov-2001 #text_change 14-Dec-2001
C.Accession: AFISIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-317 <CHES.
A;CROSS-references: EMBL:UZ0808; NID:g1184120; PID:g1184121
A;Experimental source: strain RWilcz cv. Berken; tissue type hypocotyl; clone MI C;Superfamily: alcohol dehydrogense; long-chain alcohol dehydrogense; bomology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: lin0622
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                    oxidoreductase homolog lin0622 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL592022; PIDN:CAC95854.1; PID:g16413062; GSPDB:GN00178
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 HVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 VVFDTWGGQIE-TBSYDVLKEG-TGRLVSIVGISNE---DRAKEKNVTAN-GIWLQPNGE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAVVIENYGGKEELKEKEVAMPKAGKNOVIVKEVATSINPIDWKLREGYLKOMMDWEFPI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Vigna radiata (mung bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAVIIE---GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWK----HIAYKIGPE-GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILGCDIAGTVVXLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 THSTADEISEGPVKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 BI-------LLGATRFP-----ASPEYHEATVKFVKFIN 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLKKLGELLANKTVKPIVGAT-PPFSEKGVPDAHALSETHHAVGKIVISFN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.5%; Score 260; DB 2; Length 313; Best Local Similarity 28.8%; Pred. No. 5.4e-12; Matches 101; Conservative 60; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - mung bean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-313 <GLA>
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AE1151
oxidoreductase homolog lmo0613 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Decies: Listeria monocytogenes
C;Decies: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Species: Listeria monocytogenes
C;Decies: Listeria monocytogenes
C;Decies: Listeria, Respecies.
C;Dominguez-Bernal, G;Duchaud, E;Durand, L;Dussurget, O;Entian, K.D.;Fsihi, H.D.;Jones, L.M.; Karst, U.Science 294, 494-9652, 2001
A;Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;Malok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Attle: Comparative genomics of Listeria species.
A;Attle: Comparative genomics of Listeria species.
A;Accession: AE1151
A;Accession: AE1151
A;Accession: AE1151
A;Accession: BNA
A;Residues: 1-313 <GLA>
A;Cross-references: GB:NC 003210; PIDN:CAC98691.1; PID:gl6410002; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: Imo0613
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 THSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 TAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQ 239
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DBISEGPVKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQ 184
                                                                                                                                                 GITFPADPEARRATIEFVKFINPKISDGQIHHIPARVYKNGLYDVPRILEDIKIGKNSGE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 VVFDTMGGQIB-TDSYDVLKEG-TGRLVSIV----GISNEDRAKEKAVTATGIWLQPNG 261
                              QLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDA 244
                                                                                                                                                                                                                                VGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLG 304
                                                                                                                                                                                                                                                                                                                                                305 ATRFPASPEYHEATVKFVKFINPHLANGDIHHMAIKVFSNGLDDVPALTEGIKEGKNKAV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 KAVIIE----GDKAVVKTDVSVPELKEGTALVKVBAVAGNPTDWK-----HIAYKIGPE-GS 59
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29.0%; Pred. No. 2.7e-12;
ive 56; Mismatches 120; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLVAVL 367
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Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-324 <STO>
A;Cross-references: GB>AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04082.1; GSPDB:GN001
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quinone oxidoreductase BH0363 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: C83695
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                   zinc-binding oxidoreductase Atu5324 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: Atu5324
A;Genome: plasmid
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AYKIGPEGS---ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 RVYPPLFYKSNLTHSTADEISEGPVK-NFESAASLPVSLTTAG---VSLCHHLGSKME-- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 TV-------PASELALKPAGIDHIQAAGAPMSLLTAWQFLVDLGHDAPNPFQSF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 WHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 RHSPIPLQGKIVLVNGAGGGVGHLAIQLAKWRGAH--VIAVASGKHEALLRALGADQIID 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 EAMMIEMMKAVRLHEFGGPEVLSYEEAPRPVAASGEVLVRVHAAGINPPDLYLRDGYRTL 72
                                                                                                                                                                                                                                                                                                 C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AF3199
        168 QLAKHVYGASKVAATASTEKLELVRSLGADLAIDYTKEN-IEDLPDKY----DVVFDAIGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 KAVIIEGDKAVVKTDVSVPEL-------KEGTALVKVEAVAGNPTD-----WKHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 YHDAGVIEQIKSKYPNLQHVIDAVGSED 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 YTKTAA----ETAAEDVDLVIDAVGGSN 260
                                                              248 EDS----IPEAYKVTA 259
                                                                                                                    224 CDKAVKVÍKEGGKVVA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <KUR>
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Best Local S:
Matches 80
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C;Accession: E86301
R;Theologis, A.; Ecker, J.R.; Pelm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Sowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: E86371
A;Accession: E86371
A;Accession: E86371
A;Accession: E86371
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                         PLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHT- 170
                                                                                                                                                                                                                                                                                                                                                                                    171 -HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QIKSKYPNLQHVIDAVGSED----SIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDN 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIGPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKN-GAFAEYARVYP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVG-SAVKDLKEGDEVYANVSEKALEGPKOFGSLAEYTAVEEKLLALKPKNI----- 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DFAQAAGLPLAIETADEGLV-----RTEFSAG-----KSILVLNGAGGVGSLVI 167
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                                                                                                                                                        15 DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKI----GPEGSILGCDIAGTVV 70
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A;Rosidues: 1-309 <STO>
A;Cross references: GB:AE005172; NID:g4056456; PIDN:AAC98029.1; GSPDB:GN00141
C;Genetics:
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                                                              56;
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                                                                                                                       SVPTTOKAVIIE---GDKAVVKTD--VSVPELKEGTALVKVEAVAGNPTDWK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 VKIDITLLYRASGQEILLGATRFPASPEYHEATVKFVKFINPHLNNGDI 334
  Length 317;
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     , Score 259; DB 2; Length 31;
   Pred. No. 6.6e-12;
49; Mismatches 143; Indels
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Query Match
Best Local Similarity 28.99
Matches 101, Conservative
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quinone oxidoreductase BH0935 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Datesion: G83766
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and capacesion: G83766
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: GB.AP001510; GB.BA000004; NID:g10173440; PIDN:BAB04654.1; GSPDB:GN001
A.Experimental source: strain C-125
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Aththors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: BH0935
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
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A; Status: preliminary
A; Molecule types: DNA
A; Molecule types: DNA
A; Residues: 1.734 - KUR>
A; Cross-references: GB: AE008687; PIDN: AAL46134.1; PID: g17743901; GSPDB: GN00188
A; Experimental source: strain C58 (Dupont)
         163 AQIKPYS----RYPIWAGSSGVGVAGIQLAKAFNAFV-ITTAGNEEXAKKCKELGADLV 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 LLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 KAVIIE--GDKAVVKT-DVSVPELKEGTALVKVEAVAGNPTD-------WKHIAY
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                                                                                                                                            220 FDYHDAGVIEQIKSKY-PNLQHVIDAVG 246
                                                                                                                                                                                                   217 FNHYKDDVVKKVREVFKEGVDVVVDHIG 244
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A;Molecule type: DNA
A;Residues: 1-322 <STO>
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A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.E.; O
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A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: C70418
A/Status: presention of sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-343 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable alcohol dehydrogenase (EC 1.1.1.-) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: C70418
R;Deckert, G.; Warren, P.V.; Gassterland, T.; Young, W.G.; Lenox, A.L.; Graham,
C;Genetics:
A;Gene: BH0363
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
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C,Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C,Keywords: NAD; oxidoreductase
F,26-332/Domain: long-chain alcohol dehydrogenase homology <LADH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 FPIPDEI-----NFRIAAASPI-----VSFLSH---RLLYNVAQMERGESVLVHAAAG 148
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MTNGVGVD-----IILDSVSGSVTEKSLQCLARYGRLVHFGNSSGAİGTIKTIDLHA 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 VIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDI----TLLYRA 296
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                                                                                                                                                                                                                                                                                                                                                                                                           ch 10.1%; Score 193; DB 1; Length 343; I Similarity 28.7%; Pred. No. 6.7e-07; 77; Conservative 43; Mismatches 94; Indels 54; Gaps
                                                                                                                                                                                                                                                                                                                                                         KAVIIE---GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL---
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       99
                                                                                                                                                                        Query Match 10.8%; Score 208; DB 2; Length 324; Best Local Similarity 26.4%; Pred. No. 4.6e-08; Matches 90; Conservative 53; Mismatches 132; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGOEIL---LGATRFPASPEYHEATVKFVKFINPHLNNGDI 334
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Best Local S
Matches 77
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GMFLVQLGKKFGAKVIAVSRKSWLRGYGADFVVDYNEVEFKVKEITNGFWA 20HVIDAVGSEDSIPEAYKVTADSLP-ATLLEVPWTIESIPEEIRKDNVKIDITLL	MSVPTTQKAVI
C;Genetics: A;Genome: plasmid C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology Ouery Match Best Local Similarity 27.5%; Pred. No. 1.8e-06; Matches 90; Conservative 40; Mismatches 123; Indels 74; Gaps 14; A; ExvIledbravy. B KAVIEGDRAVVTDVSVPELKEGTALVXVEAVAGNPTDWKHAYKI 54        :	RESULT 13 Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods Bloods

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                                                  W.; Perry, M.; Gordon-Kamm,
Science 294, 2317-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Part, E.M.
A;Artile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Recession: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNL--QHVIDAVG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 KLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYK--SNLTHSTADEIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 EGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPOHTHPLLIWGGATAVGQQLIQ 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDW--KHIAYK-IGPEGSILGCDIAGTVV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 9.0%; Score 173.5; DB 2; Length 3
1 Similarity 25.5%; Pred. No. 1.8e-05;
94; Conservative 44; Mismatches 146; Indels
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303 LEKPNNGLR 311
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Best Local Si
Matches 94;
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RESULT 16
E86714
quinome oxidoreductase qor [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: E86714
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Tatle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Accession: E86714
A;Accession: E86714
A;Molecule type: DNA
A;Residues: 1-328 cSTO>
A;Cross-references: GB:AE005176; PID:g12723629; PIDN:AAK04815.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: qor
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Gaps 11;

44;

Length 328;

9.0%; Score 173; DB 2; Length 328 28.8%; Pred. No. 2e-05; tive 43; Mismatches 91; Indels

Query Match Best Local Similarity 28.8% Matches 72; Conservative

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8 KAV-IIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGS----IL 61

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C;Accession: B83742

T;Takkami, H.; Naksone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira. Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete genome sequence of the The Title: Nateference number: A83650; MUID:20512582; PMID:11058132

A;Steatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04457.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: BH0738
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                               63 LGWDASGTVVEVGEDCKL-FKLGDEVP---YSGSIT--RQGTYSBYHLVDERIVGHKP-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 NLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWG 177
                                                                                                                                                                                                                                                                                       178 GATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVPDYHDAGV--IEQIKSKY 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KRITHA------EAAALPLTTTAWEALFERLRINSDDVEGNKEKT--IL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 IWGGATAVGQQLIQVAKHINAYTKIVTVASKKHE-KLLKSYGADDVFDYHDAGVIEQIKS 233
                                                                              62 GCDIAGTVVKLGPNASTDLKVGDTGF--GFVHGASQTDPKNGAFABYARVYPPL--FYKS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 YKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLL 174
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alginate lyase BH0738 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Peb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VPTTOKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYK--IGPEGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.0%; Score 172.5; DB 2; Best Local Similarity 28.0%; Pred. No. 2.3e-05; Matches 69; Conservative 45; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                            210 VDYILILNAV 219
                                                                                                                                                                                                                                                                                                                                                                                              236 PNLQHVIDAV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLINE 215
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C;Accession: AH3289
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessci Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitenssi A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T10203
C;Accession: T10203
K;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16991
A;Accession: T10203
                                                                                                                                                                                                                            NADPH2:quinone reductase (BC 1.6.5.5) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #text_change 03-Jun-2002 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 4
A;Introns: 22/3; 70/1; 100/3
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
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C,Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C,Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE008917; PIDN: AAL51483.1; PID: 917982195; GSPDB: GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 TDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFES 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AAAIPETFFTVWHNVFERGGLK------EGEVFLVHGGSSGIGTTAIQLAKAFGA-T 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 KIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKY--PNLQHVIDAVGSEDSIPEAY 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F2SG13.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 VITTAGSKEKCDACVKLGADRAINYHEEDFVAVVKEMTGGKGVDVILDMVGG-DYVERNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 SVPELKEGTALVKVEAVAGNPTDWKHIAYKIG----PEGS--ILGCDIAGTVVKLGPNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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A;Residues: 1-329 <BEV>
A;Cross-references: EMBL:AL079349; GSPDB:GN00062; ATSP:F25G13.100
A;Experimental source: cultivar Columbia; BAC clone F25G13
      190 AKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKS 233
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.9%; Score 170.5; DB 2; Best Local Similarity 27.8%; Pred. No. 3.2e-05; Matches 68; Conservative 33; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-336 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 KVTAD 260
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197481
probable oxidoreductase (PA3567) [imported] - Agrobacterium tumefaciens (strain C58, Cer probable oxidoreductase (PA3567) [imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97481
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 394, 231-3238, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                           A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD269
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-338 <KUR>
A;Residues: 1-338 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42010.1; PID:g17739384; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
A;Gene: Atu0996
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 PNASTDLKVGDTGF--GFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .-----HLVDERIVGAK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 VK--NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-338 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86805.1; PID:g15156011; GSPDB:GN00169
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1 Similarity 28.6%; Pred. No. 2.7e-05;
64; Conservative 36; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 AKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKS 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.9%; Score 171.5; DB 2
larity 28.6%; Pred. No. 2.7e-05;
Conservative 36; Mismatches 89
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A; Map position: circular chromosome
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64; Conserva
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Matches 64; Conserva
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C;Species: Vibrio cholerae.
C;Species: Vibrio cholerae.
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 24-May-2001
C;Accession: A82309
C;Accession: A82309
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I. R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004141, GB:AE003852; NID:g9654976; PIDN:AAF93720.1; GSPDB:GN001:
A;Experimental source: serogroup O1; strain N16961; blotype E1 Tor
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                     quinone oxidoreductase VC0552 [imported] - Vibrio cholerae (strain N16961 serogroup Ol)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quinone oxidoreductase qor [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                         257 IIAFLGGATAEKVDLRPIMVKRLIVTGSTWRPRTADEKRAIRDELVEQVWPLIESGKVAP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L----GCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAPAEYARVYPPLFYK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNLQHVIDAVGSEDSI-----PEAYKVTADSLPATLL------EVVPMTIESIPE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EVDVLIDLVGGEAALDALKCLKDNARVITVPTLTAELICEKAKLLGFEATGMLVDPNPE 288
                             --LLGATRPPASPEYHEA-TVKFVKPINPHLNNGDIHH 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 DKAVVKTDVSVPEL-----KEGTALVKVEAVAGNPTDWK---HIAYKIGPEGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 SNLTHSTADEISEGP-VKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.5%; Score 164; DB 2; Length 337; Best Local Similarity 25.8%; Pred. No. 9.9e-05; Matches 82; Conservative 47; Mismatches 111; Indels 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 EIRKDNVKIDITLLYRAS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLD-----TMLYMVS 298
                             289 DITLLYRASGOEI ----
                                                                                                                                                    317 VINRVFT--LEEV 327
                                                                                                                       337 MNIKVFSNGLDDV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-337 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A82309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: VC0552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable quinone oxidoreductase [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C; Accession: F97459
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Luu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Artile: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUD:21608551; PMID:11743194
A; Retenus: preliminary
A; Moleçule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AjGene: AGR C 1508
A;Map position: circular chromosome
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                            -PEGS--ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 LFYKSNLTHSTADEISEGPVKNFES--AASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEIS 128
                                                                                                                                                                                                                                                                                   EGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQ 188
                                                                                                                                                                                                                                                                                                                 AA-----EAAALPVAGLTALQALTNPAGLKLD---GTGKKAN-ILVTAASGGVGHYAVQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PNLQH---VIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNV 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 PFSVFEPNLSENGKVIDITPGPNAM---WTYAVKKITMSKKQLVPLLL--IP---KAENL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1-348 «KUR»
A,Cross-references: GB:AE007869; PIDN:AAK86631.1; PID:g15155807; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKSKY--PNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---FEKNLAALAKDGCLS 256
                                                                                                                                                                                                                                      VVEVGSGVK-NFKAGDKVVAVLSHLG-----GGGLAEFA-----VATEKLTVKRPQEVG 124
                                                                                                                            2 SVPTTQKAVIIE---GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIG--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLPETMRRIDLPSHGGPEVMQSSKAPLPKPARGEILVKVBAAGVNRPD---VAQRQGIYP 73
                                                                                                                                                                                                                                                                                                                                                                                 VARHINAYTKI VTVASKKHEKLLKSYGADDVFDY---HDAGVIEQIKSKY-----
                                                                                              14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGP----EGSILGCDIAGT
                                                      Gapa
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                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 348;
    DB 2; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 164.5; DB 2; Length 23.6%; Pred. No. 9.5e-05; Live 62; Mismatches 136; Indels
                                               56; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFMVNLVKEGKVKTVI--DSKHPLS----KAEDAWAKSIDGH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 KIDITLLYRASGQEILLGATRFPASPEYHEATVKFVKFINPH
  8.6%; Score 164.5; DB 2 23.4%; Pred. No. 8.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 VKSETGGKGVDVVLDMIGA----AY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.6*
Matches 88; Conservative
                                                 Conservative
                        Similarity
Query Match
Best Local S:
Matches 80,
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A;Cross-references: GB:L31521
C;Comment: This protein is present at low (enzymatic) levels in this species, in contrast
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C;Species: J.-Dec-1993 #sequence_revision 07-Jul-1995 #text_change 11-Jun-1999
C;Accession: PN0448; A54672
C;Accession: PN0448; A54672
R;Gonzalez, P.; Rao, P.V.; Zigler Jr., J.S.
Biochem. Biophys. Res. Commun. 191, 902-907, 1993
A;Title: Molecular cloning and sequencing of zeta-crystallin/quinone reductase cDNA from A;Reference number: PN0448; MUID:93221534; PMID:8466529
A;Accession: PN0448
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A; Residues: 1-329 <GOND,

A; Residues: 1-329 <GOND,

A; Residues: 1-329 <GOND,

A; Experimental source: liver

A; Note: translation of initiator Met is not shown; the authors translated the codon ATC

B; Gonzalez, P.; Rao, P.V.; Zigler Jr., J.S.

Genomics 21, 317-324, 1994

A; Title: Organization of the human zeta-crystallin/quinone reductase gene (CRYZ).

A; Reference number: A54672; MUID:94375054; PMID:8088025
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: eye lens; NADP; oxidoreductase
F;33-318/Pomain: long-chain alcohol dehydrogenase homology <LADH>
F;33-318/Region: beta-alpha-beta NADP nucleotide-binding fold
                                                                                                                                                                                                                                                                                                                                                                             161 WATHLGVRV-ITTVSTAEKAKLSKDAGADVVLDYPEDAWQFAGRVRELIGG-TGVQAVYD 218
                                                                                              72 LGPN---ASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEIS 128
                                                                                                                                                                                                                                                                                                    129 EGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 NASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK- 133
                                                                                                                                                            24 LRSDIAVPIPKDHQVLIKVHACGVNPVE-TYIRSGTYSRKPLLPYTPGSDVAGVIEAVGD
GGPGVLRHVDQPQPQPGHGELLIKAEAIGVNFIDTYFRSGQYPRELPFVIGSEVCGTVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 VAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHD----AGVIEQIKSKYPNLQHVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 VKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL----GCDIAGTVVKLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ceta-crystallin / quinone reductase (NADPH) (EC 1.6.-.-) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.4%; Score 161; DB 1; Length 329; Best Local Similarity 24.8%; Pred. No. 0.00016; Matches 73; Conservative 50; Mismatches 95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 AVGS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 GVGA 222
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A;Residues: 1-37 <GO2>
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A7081.
R;Cole, S.T.; Brosch, R.; Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devihn, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 339, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-228 «COL»
A;Cross-references: GB:AL021184; GB:AL123456; NID:93261498; PIDN:CAA15984.1; PID:9279138
                               A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8. A,Accession: A12677, MUID:21608550; PMID:11743193
A,Accession: A12677
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-327 < KURP.
A,Residues: 1-327 < KURP.
A,Experimental source: strain CS8 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Gene: gor
A, Map position: circular chromosome
C, Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
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C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
F;25-318/Domain: long-chain alcohol dehydrogenase homology «LADH»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 LIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKY--PNLQHVID 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|| | ::|| : |:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 SEGPVKNFES--AASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::: | | | :::
|-----FEKNLAALAKDGCLSIIAFLGGATAEKVDL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 AVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEI-- 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIG----PEGS--ILGCDIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LLGATRFPASPEYHEA-TVKFVKFINPHLNNGDIHHMNIKVFSNGLDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 8.4%; Score 162; DB 2; Length 327; I Similarity 24.0%; Pred. No. 0.00013; 86; Conservative 57; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 MIGA-----ÀY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 86
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14;

76; Gaps

74 82 194 NAY-TKIV-TVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSI 251

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134 NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHI 193

ò 셤 ò

13;

95; Indels 41;

Query Match

8.4%; Score 161.5; DB 2; Length 328;
Best Local Similarity 29.5%; Pred. No. 0.00015;
Matches 72; Conservative 36; Mismatches 95; Indels 41

GDKAVVK-TDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE-GSILGCDIAGTVVK

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<u>:</u> <u>:</u>

.-----PEKL 121

82

16;

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RiGonzalez, P.; Hernandez-Calzadilla, C.; Rao, P.V.; Rodriguez, I.R.; Zigler Jr., J.S.; E Mol. Biol. Evol. 11, 305-315, 1994
A;Title: Comparative analysis of the zeta-crystallin/quinone reductase gene in guinea pig A;Reference number: A54932; MUID:94224126; PMID:8170370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: Requence extracted from NCBI backbone (NCBIN:147625, NCBIP:147626)
A;Note: translation of initiator Met is not shown
R;Joernvall, H.; Persson, B.; du Bois, G.C.; Lavers, G.C.; Chen, J.H.; Gonzalez, P.; Rao,
PEBS Lett. 322, 240-244, 1993
A;Title: zeta-Crystallin versus other members of the alcohol dehydrogenase super-family.
A;Reference number: S42272; MUID:93252077; PMID:8486156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: annotation
C; Comment: This protein is a major soluble protein of the lens in this species and is exp
C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C; Keywords: eye lens; NADP; oxidoreductase
F;33-320/Domain: long-chain alcohol dehydrogenase homology «LADH»
F;152-181/Region: beta-alpha-beta NADP nucleotide-binding fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 VSA-PKKGDRVFCY-----STVSGGYAEPALAADDTIYP-----LPB- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 DFRQGAAIGIPYFTA----CRAL----FHSARAKAGESVLVHGASGGVGLAACQIAR-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 ASTDLKVGDTGFGFVHGASQTDPKNGAFAEYA-----RVYPPLFYKSNLTHSTADEISEG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 PVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 -TLNFRQGAALGIPYFTA----CRAL----FHSARARAGESVLVHGASGGVGLATCQIA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 KHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDS 250
                                                                                                                                                                                                                                                                                                                    75 NASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK- 133
                                                                                                                                                                                                                                                                                                                                                                                         83 DVSA-FKKGDRVF-----TTSTISGGYAEYALASDHTVYRL-------PEKL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQOLIQVAKHI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 VKTDVSVPELKEGTALVKVEAVAGNPTDW--KHIAYKIGPEGSIL-GCDIAGTVVKLGPN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 LQSDVVVPVPQSHQVLIKVHACGVNPVETYIRSGAYSRKPALPYTPGSDVAGIIESVGDK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zeta-crystallin / quinone reductase (NADPH) (EC 1.6...) - mouse
C;Species: Num musculus (house mouse)
C;Date: 25-Apr-1995 #sequence_revision 07-Jul-1995 #text_change 11-Jun-1999
C;Accession: A34932; S42273
                                                                                                                                                                                                                      24 VQSDVAVPIPKDHQVLIKVHACGINPVB-TYIRSGTYTRIPLLPYTPGTDVAGVVESIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 NAY-TKIV-TVASKKHEKLLKSYGADDVPDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 - AYGLKVLGTAGTEEGQKVVLQNGAHEVFNHRDAHYIDEIKK------SIGEKG--
                                                                                                                                                                              19 VKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL----GCDIAGTVVKLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-331 <GON>
A;Crose-references: GB:S70056; NID:g546493; PIDN:AAB30620.1; PID:g546494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------SCGRVIIVG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 PEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 331;
                                    Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.3%; Score 158.5; DB 1;
Best Local Similarity 22.4%; Pred. No. 0.00025;
Matches 72; Conservative 53; Mismatches 119;
                                    Query Match 8.3%; Score 159; DB 1; Best Local Similarity 24.2%; Pred. No. 0.00023; Matches 71; Conservative 50; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: liver
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                                                                                                                                                                                                                                    AC1856
hypothetical protein all0412 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Accession: AC1858
C;Accession: AC1858
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; WUID:21S95285; PMID:11759840
A;Accession: AC1858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 < KUR.
A;Cross-references: GB:BA000019; PIDN:BAB72370.1; PID:g17129757; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zeta-crystallin / quinone reductase (NADPH) (EC 1.6.-.-) - guinea pig
N;Alternate names: quinone reductase (NADP)
C;Species: Cavia porcellus (guinea pig)
C;Accession: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jun-1999
C;Accession: 350230
Gene 78, 215-24, 1989
A;Title: Zeta-crystallin, a novel protein from the guinea pig lens is related to alcohol A;Reference number: JS0230; MUD:89378748; PMID:2777081
A;Accession: JS0230
A;Accession: JS0230
A;Accession: JS0230
A;Accession: JS0230
A;Accession: JS0230
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A; Experimental source: strain 13/N
A; Experimental source: strain 13/N
A; Note: the sequences of seven fragments (79-98, 95-106, 106-114, 209-215, 264-275, 291-A; Note: this protein is distantly related to mammalian and yeast alcohol dehydrogenases C; Comment: This protein constitutes about 10% of the water-soluble proteins of the lens. C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C; Keywords: eye lens; NADP; oxidoreductase F;33-318/Domain: long-chain alcohol dehydrogenase homology ciaDH>
F;152-181/Region: beta-alpha-beta NADP nucleotide-binding fold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Genetics:
A,Gene: all0412
C,Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 STDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYK--SNLTHSTADEISEGPVKN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHIN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --EAATVPVAGGTAWAALITR-----ANLQVGETVLIHGGAGGVGTFAIQIAKAAG 168
-AYGLKILGTAGTEEGQKIVLQNGAHEVFNHREVNYIDKIK-KY------VGEKG-- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPE---GSILGCDIAGTVVKLGPNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 -RDFOVGDE----VYYAIPHELGGGANAEYHAFPSSMIAKKPNNISHL-------
                                                                                                                252 PEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLGA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 159.5; DB 2; Length: 30.0%; Pred. No. 0.0002; tive 25; Mismatches 87; Indels
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Best Local Si
Matches 63
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251 IPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLGATRFPA 310
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255 EINPRDTMAKETSIIGVSLSS 275
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hypothetical protein F39B2.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T21985
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Ribobson, R.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19498
A;Reference number: Z19498
A;Reteaus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Redidues: 1-328 «WIL»
A;Cross-references: EMBL: Z92834; PIDN: CAB07384.1; GSPDB: GN00019; CESP: F39B2.3
A;Experimental source: clone F39B2

C;Genetics: A;Gene: CESP: F39B2.3

A;Map position: 1 A;Introns: 118/1; 145/3 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology Length 328;

5 TTQKAVIIB--GDKAVVK-TDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGS-- 59 50; 90; Indels Query Match 8.2%; Score 157; DB 2; Best Local Similarity 26.7%; Pred. No. 0.00032; Matches 67; Conservative 44; Mismatches 90; 셤

> ò g

114 ------ELPEG--VSFBEGASLGVPYLTAYRALFHLAGAKT-------GDVILV 152 116 KSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLI 175 ò g 176 WGGATAVGQQLIQVA--KHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKS 233 

ö 셤 234 KYP-NLQHVID 243 ò

|| |: : 210 DYPGGFNHIFE 220

Search completed: January 10, 2004, 10:08:01 Job time : 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 10, 2004, 08:41:33 ; Search time 23 Seconds (without alignments) 756.517 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-081-644-2 1920 1 MSVPTTQKAVIIEGDKAVVK......ALTEGIKEGKNKNVKYVARL 370

Scoring table:

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

127863

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 90 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

W	Description		P54007 saccharomyc			Q9zucl arabidopsis			cavia				-							P20369 kluyveromyc		O58389 pyrococcus		P12311 bacillus st	-	-			_	Q8e8j1 shewanella	P19333 torpedo cal	6	P49384 kluyveromyc	P38230 saccharomyc
SUMMARIES	ΩI	YNN4 YEAST	YL60 YEAST	YCZ2 YEAST	TOXD_COCCA	CORL ARATH	ADH2_CANAL	OOR HUMAN	OOR_CAVPO	OOR_MOUSE	COR LEIAM	YM27_YEAST	P1 ARATH		ADH2_PICST	ADH1_PICST	QOR BOVIN	QOR_LAMGU	P2_ARATH	ADH1 KLULA	ADH1 CANAL	TDH_PYRHO	TDH_ECOL6	ADH1_BACST	TDH_PYRAB	TDH_ECOS7	TDH SHIFL	ADH2_KLUMA	TDH ECOLI	TDH_SHEON	VATI_TORCA	TDH_PYRFU	ADH3 KLULA	OOR YEAST
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	Score	65.	1021.5	1015.5	370.5	ın	175.5	191	159	158.5	155	154	153.5	153.5	152.5	149.5	148	148	14	4	ë	マ		141.5	141.5	141	141	140.5	140	140	14	37	٠	132
	Result No.	-	7	m	4	ហ	ø	7	89	o	10	1	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53	30	31	32	33

946	hart line	Domination of C	3 kluvveromv	6 rhizobium	8 bac	4 salmonell	52 BB	11 saccharomy	10 saccha	<u> </u>	2.	":		: ≃	:::		9	_	:	덮	0	12 mus muscu	12 yersinia	ogenicado	76 baci	2 Bchizosacc	~ ~	s rnizobium	2 5	: 2	. 10	9	5	2		2 3	2 .	٠.	10 entamoeba	12 saccharopo	io pasteur	6 ovis aries	12 vibrio vu	14 rhodobact	33 salmonella	7 rhizobium	14 080	// arabidopsi	7 cecherichi	77 saccharomy	94 98	petroselin	•
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## ALIGNMENTS

		•				e)	Hypothetical 41.2 kDa protein in FPR1-TOM22 intergenic region.			Rukarvota: Mingi: Ascomvoota: Saccharomvootina: Saccharomvoete
		376 AA.			e update)	ion updat	PR1-TOM22		yeast).	ha romycot
		PRT;		ted)	Bequence	annotat	ein in Fl		Baker's	that Sacci
		STANDARD;		34, Crea	34, Last	34, Last annotation update	kDa prot	OR N1847.	evisiae (	Ascomyco
				96 (Rel.	96 (Rel.	96 (Rel.	cal 41.2	R N1214	усев сех	Finner:
RESULT 1	YNN4 YEAST	YNN4 YEAST	P53912;	01-OCT-19	01-OCT-1996 (Rel. 34, Last sequence update)	01-OCT-19	Hypothetic	YNL134C OR N1214 OR N1847.	Saccharomyces cerevisiae (Baker's yeast).	Eukarvota
RES	XXX	Ω	Ą	Į	H	ŭ	DE	Z	SO	Ö

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                                                                                                                                                                   MEDLINE=97313267; PubMed=9169871;
A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Johnston M., Hillier L., Riles L., Duesterhoeft A., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Louis E.J., Messenguy F., Mewes H.-W., Miooga T., Moest D., A., Mueller-Auer S., Nentwich U., Obermaler B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Voncendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D., T. The nucleotide sequence of Saccharomyces cerevisiae chromosome XII."; Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LGCDAAGQIVKLGPAVNPKDFSIGDYIYGFIHGSSVRFPSNGAFAEYSAISTVVAYKSPN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 NLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 ELKFLGEDVLPAGPVRSLEGVATIPVSLTTAGLVLTYNLGLDLKWEPSTPQRKGPILLWG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 GATAVGOSLIQLANKINGFTKIIVVASRKHEKLIKEYGADELFDYHDIDVVEQIKHKYNN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 ISYLVDCVANQDILQQVYKCAADKQDATIVELKNLTEENVKKENRRQNVTIDIIRLYSIG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 GQEILLGATRFPASPEYHEATVKFVKFINPHLNNGDIHHMNIKVFSNGLDDVPALTEGIK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 LQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSVPTTQXAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSI
     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: BELONGS TO THE YCR102C/YLR460C/YNL134C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.2%; Score 1021.5; DB 1; Length
Best Local Similarity 51.7%; Pred. No. 2.1e-66;
Matches 193; Conservative 67; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 376 AA; 41127 MW; 00139949423862F1 CRC64;
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InterPro; IPR02085; Adh zn family.
Pfam; PF00107; ADH_zinc_N; I.
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                                                              NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SO4 NDVPFGTFTLPADPEYKEAAIKFIKFINPKINDGEIHHIPVKVYKNGLDDIPOLLDDIKH 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEILLGATRFPASPEYHEATVKFVKFINPHLANGDIHHMNIKVFSNGLDDVPALTEGIKE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SVPTTQKAVIIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                      Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
-! SIMILARITY: BELONGS TO THE YCR102C/YLR46OC/YWL134C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 41.1 kDa protein ON CDC91-PAU4 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 AA; 41164 MW; AE39BBCDA46C33B9 CRC64;
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGD; S0005078; YNL134C.
InterPro; IPR002085; Adh zn family.
Pfam; PF00107; ADH zinc_N; I.
                                                                                                                                              MEDLINE=96109932; PubMed=8619318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z46843; CAA86891.1; -. EMBL; Z71410; CAA96016.1; -.
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Matches 201; Conservative
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                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
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P54007;
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YL60_YEAST
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul
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MEDLINE=21016719; Pubmed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.0%;
Matches 102; Conservative
                                                                                                                                                                                                   STRAIN=ATCC 90305 / SB111,
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Arabidopsis thaliana
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLIQLANKLNGFTKIIVVASRKHEKLLKEYGADQLFDYHDIDVVEQIKHKYNNISYLVDC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 VANQNTLQQVYKCAADKQDATVVELTNLTEENVKKENRRQNVTIDRTRLYSIGGHEVPFG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVVKLGPNAS-TDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKS--NLTHSTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OIVKLGPAVDPKOPSIGDYIYGFIHGSSVRPPSNGAFAEYSAISTVVAYKSPNELKFLGE 121
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                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                Grivell L.A., de Haan M., Maat M.J.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE YCR102C/YLR460C/YNL134C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0000699; YCR102C.
InterPro; IPR002085; Adh.zn family.
Pfam; PF00107; ADH.zinc.N. I.
SEQUENCE 368 AA; 40121 MW; 0BEE4FB4DB04AF8B CRC64;
                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
40.1 kDa protein in GIT1-PAU3 intergenic region.
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
  368 AA
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X59720; CAA42244.1; -. PIR; S19414; S19414.
STANDARD; .
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194; Conservative
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TOXD COCCA
P54076;
01-0CT-1996 (Re
01-0CT-1996 (Re
28-FBB-2003 (Re
TOXD protein.
YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 IDAVGSEDS--IPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DYAGIVESVGRSVKKPFKKGDRVCGFAHGGNAVFSDDGTFAEVITV-----KGDIQAWI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 FDTISIDVSARFCDRAMSTEGGEYSALLDV-----SIARTNISSRWTLAYTVLGE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TPQKAIVTEAPHRARLVSDRLIPKLRDDYILVRTVSVALNPTDWKHI-LRLSPPGCLVGC 60
                                                                                                                                                                                                                                                                      Cheng Y.-Q., Ahn J.-H., Walton J.D.;

ToxD, a gene cloned from a HC-toxin producing strain of Cochliobolus

"ToxD, a gene cloned from a HC-toxin biosynthesis.";

Submitted (CT-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: UNIQUE TO ISOLATES THAT MAKE THE CYCLIC PEPTIDE HC-
TOXIN, BUT HAS NO ROLE IN TOXIN BIOSYNTHESIS.

-!- SIMILARITY: BELONGS TO THE YCRI02C/YLR460C/YNL134C FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X92391; CAA63129.1; -. Interpret PRO02085; Adh an Eamily. Pro0107; Abla zinc. N_1.1. SEQUENCE 297 AA; 32549 MW; 0PFB18C93E4521A1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%; Score 370.5; DB 1; 34.0%; Pred. No. 1.2e-19; tive 53; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outhone exidoreductase-like protein At1923740
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Candida albicans (Yeast)
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                                                 NCBI_TaxID=5476;
                                                                                                                                                                                                                      family.
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                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are perfictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb-sib.ch).
71 KLGPNASTDLKVGDTGFGFVHGASQTDPKN-GAFAEYARVYPPL--FYKSNLTHSTADEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVG-SAVKDLKEGDEVYANVSEKALEGPKQFGSLAEYTAVEEKLLALKPKNI------ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 SEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 -----DFAQAAGLPLAIETADEGLV----RTEFSAG-----KSILVLNGAGGVGSLVI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ...: |||:|| || || DVLKLESNIVVPEIKEDQVLIKVVAAALNPVDAKRRQGKFKATDSPLPTVPGYDVAGVVV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKI----GPEGSILGCDIAGTVV
                                                                                                                                                                                                                                              Nature 408:816-820(2000).
-!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family. Quinone oxidoreductase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.2%; Score 254; DB 1; Length 309; 32.8%; Pred. No. 3.3e-11; ive 35; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Zinc; NAD. SEQUENCE 309 AA; 32775 MW; EC328042771BEEEG CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; ACUU3270,
PIR; B86371, E86371.
SWISS-2DPAGE; Q92CT; ARATH.
INTERPRO; IPR002085; Adh zn. family.
InterPro; IPR002085; Adh zn. family.
InterPro; IPR002085; Adh zn. family.
InterPro; IPR002085; Adh zn. family.
Pfam; PF00107; ADH zinc N; 1.
PROSITE; PS01162; QOR ZĒTA_CRYSTAL; FALSE_NEG.
PROSITE; PS01162; AND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADH2 OR CA41C10.04.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC005990; AAC98029.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 EDS----IPEAYKVTA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 CDKAVKVIKEGGKVVA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Conservative
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Best Local Similarity
Matches 84; Conserval
                                                                                                                                                                                                                                    thaliana.";
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ID ADH2_C

AC 094038

DT 16-OCT

DT 16-OCT

DT 15-SEP

DE Alcoho

GN ADH2_O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 ------NGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------LPAGAKISTPVFDAVIK 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 CAEADLSGYTHDGSFQQYA-----TADAV------QAARIPAGTDLA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 GyS--LCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 HEKLLKSYGADDVFDY-HDAGVIEQIKSKYPNLQH-VIDAVGSEDSIPEAYKVTADSLPA
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                                                                                                                                                                                                            Taylor K., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSVPTTQKAVIIE--GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTD---WK---HIAY
                                                                                                                                                                                                                                                                                                                                                -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
-1- SUBUMIT: Homoterramer (By similarity).
-1- SUBCELLUIAR LOCATION: Cytoplasmic (Probable).
-1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113;
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SIMILARITY)
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ZINC 1 (CATALYTIC) (BY SIMI
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMI
3D6867538522ADCF CRC64;
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InterPro; IPR00328; ADH zinc.
InterPro; IPR002085; Adh zin family.
Pfam; PF00107; ADH zinc N; I.
PROSITE; PS00059; ADH ZINC; I.
Oxidoreductase; Zinc; Metal-binding; NAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENOMICS 21:317-324 (1994).

-I- FUNCTION: DOES NOT HAVE ALCOHOL DEHYDROGENASE ACTIVITY. BINDS NADP AND ACTS TRROUGH A ONE-ELECTRON TRANSPER PROCESS.

ORTHOQUINONES ARE THE BEST SUBSTRATES. MAY ACT IN THE DETOXIFICATION OF XENOBIOTICS.

-I- CATALYTIC ACTIVITY: NADPH + quinone = NADP(+) + semiquinone.

-I- SUBUNIT: HOMOCETAME.

-I- SUBUNIT: HOMOCETAME.

-I- SUBCELLULAR LOCATION: Cytoplasmic.

-I- SINILARITY: BELOIGS to the zinc-containing alcohol dehydrogenase.
                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-Crystallin).
                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94375054; PubMed=8088825;
Gonzalez P., Rao P.V., Zigler J.S. Jr.;
"Organization of the human zeta-crystallin/quinone reductase gene
(CRYZ).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93221534; PubMed=8466529;
Gonzalez P., Rao P.V., Zigler J.S. Jr.;
"Molecular cloning and sequencing of zeta-crystallin/quinone
reductase cDNA from human liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 329;
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24.8%; Pred. No. 0.00018;
ive 50; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 AA; 35206 MW; 68C1828911486D4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 191:902-907(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family. Quinone oxidoreductase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002085; Adh.zn.family.
InterPro; IPR002364; QOR_zeta_crystal.
Pfam; PF00107; ADH_zinc_N; 1.
PROSITE; PS01162; GOR_ZETA_CRYSTAL; 1.
Oxidoreductase; NADP; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, L13278; AAA36536.1; -.
EMBL, L31526; AAK40311.1; -.
EMBL, L31521; AAK40311.1; JOINED.
EMBL, L31522; AAK40311.1; JOINED.
EMBL, L31523; AAK40311.1; JOINED.
EMBL, L31524; AAK40311.1; JOINED.
EMBL, L31525; AAK40311.1; JOINED.
PIR; PN0448; PN0448.
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GO; GO:0007601; P:vision; TAS.
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Best Local Similarity 24.8
Matches 73; Conservative
                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P28304; 1QOR.
Genew; HGNC:2419; CRYZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                                                         QOR_HUMAN
Q08257;
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                        | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 
RESULT 7
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14;

Gaps

16;

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171 -AYGLKILGTAGTEEGQKIVLQNGAHEVFNHREVNXIDKIK-KY------VGEKG-- 217
                                                                NASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK- 133
                                                                                                   NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHI 193
                                                                                                                                                    194 NAY-TKIV-TVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSI 251
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 LRSDIAVPIPKDHQVLIKVHACGVNPVE-TYIRSGTYSRKPLLPYTPGSDVAGVIEAVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=89378748; PubMed=2777081;
Rodokanaki A., Holmes R.K., Borras T.;
"Zeta-crystallin, a novel protein from the guinea pig lens is related to alcohol dehydrogenaes.";
 19 VKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL----GCDIAGTVVKLGP
                                                                                                                                                                                                                                                                                                               01-CCT-1989 (Rel. 12, Created)
01-CCT-1989 (Rel. 12, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
CUNIOND (Rel. 40, Last annotation update)
crystallin).
                                                                                                                                                                                                                   252 PEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLGA 305
                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rao P.V., Krishna C.M., Zigler J.S. Jr.; Identification and characterization of the enzymatic activity zeta-crystallin from guinea pig lens. A novel NADPH:quinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rao P.V., Zigler J.S. Jr.; "Purification of zeta-crystallin/quinone
                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                               329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reductase from guinea pig liver.";
Biochim. Biophys. Acta 1117:315-320(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
MEDLINE=93041895; PubMed=1420281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92112732; PubMed=1370456;
                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - AYGLKVLGTAGTEEGQKVVLQNGAHEVFNHRDAHYIDEIKK------SIGEKG--217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 NASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVK- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 DFRQGAAIGIPYFTA----CRAL----FHSARAKAGESVLVHGASGGVGLAACQIAR-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 NAY-TKIV-TVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 VKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGSIL----GCDIAGTVVKLGP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 VQSDVAVPIPKDHQVLIKVHACGINPVE-TYIRSGTYTRIPLLPYTPGTDVAGVVESIGN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QOR_MOUSE STANDARD; PRT; 331 AA.
P47199; Q65508; Q99L63;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gonzalez P., Hernandez-Calzadilla C., Rao P.V., Rodriguez I.R.,, Zigler J.S. Jr., Borras T.; "Comparative analysis of the zeta-crystallin/quinone reductase gene in guinea pig and mouse."; Mol. Biol. Evol. 11:305-315(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIŠSUE=Breast tumor;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 PEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Indels
                                                                                                                                                                                                                                  PIR; JS0230; CYGPZ.
HSSP; P28304; 1QOR.
InterPro; IPR002364; Adh_zn family.
InterPro; IPR002364; QOR_zeta_crystal.
Pfam; PF00107; ADH_zinc_N; 1.
PROSITE; PS01162; QOR_ZETA_CRYSTAL; 1.
Oxidoreductase; NADP; Zinc; Eye lens protein.
SEQUENCE 329 AA; 35202 MW; 1463632C672C234F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Score 159; DB 1;
24.2%; Pred. No. 0.00025;
tive 50; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94224126; PubMed=8170370;
                                                                                                                                                                                                              EMBL; M26936; AAA37035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 24.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hoptins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McEwran K.J., Malek J.A., Gibbs R.A., Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Praby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Benneration and initial analysis of more than 15,000 full-length thmen and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 VSA-FKKGDRVFCY----STVSGGYAEFALAADDTIYP-----LPE- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 PVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 VKTDVSVPELKEGTALVKVEAVAGNPTDW--KHIAYKIGPEGSIL-GCDIAGTVVKLGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 ASTDLKVGDTGFGFVHCASQTDPKNGAFAEYA-----RVYPPLFYKSNLTHSTADEISEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 130-331 FROM N.A.
STRAN=CSTBAL-66, TISSUE-Brain cortex;
MEDLINE-86216731; PubMed=8645260;
Kajiwara K., Nagasawa H., Shimizu-Nishikawa K., Ookura T., Kimura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differential screening.";
Biochem. Biophys. Res. Commun. 219:795-799(1996).
-!- FUNCTION: DDES NOT HAVE ALCOHOL DEHYROCGENASE ACTIVITY. BINDS NADP AND ACTS THROUGH A ONE-ELECTRON TRANSFER PROCESS.
ORTHOQUINONES ARE THE BEST SUBSTRATES. MAY ACT IN THE DETOXIPICATION OF XENOBIOTICS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: NADPH + quinone = NADP(+) + semiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular characterization of seizure-related genes isolated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177;
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131 133 IPY -> TWD (IN REF. 3).
331 AA; 35268 MW; 35816C043EFE16A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family. Quinone oxidoreductase subfamily.
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PROSITE; PS01162; QOR ZETA CRYSTAL; 1.
Oxidoreductase; NADP; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:88527; Cryz.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR002364; QOR_zeta_cryst
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 147 DVA-----LVTAAAGGTGQIAVQLLKHYYGCTVIGTCSSEEKAEFLKSIGCDHVINY 198
                                                                                             KTESLDGRLHELCPKGVDVVYECVGGH-TFNDAVRHVAVHARVVIIGSI6SYKSGEVVPF 257
                                                                                                                                   273 TIESIPEEIRKDNVKIDITLLYR-ASGQEILLGATRFPASPBYHEATVKFVKPINPHLNN 331
                                                                                                                                                                     SDPS------GTSVTMLLLVKSASLNGFFL------PQFHDVIPKYMANLLQYLKA 301
                                                         223 HDAGVIEQIKSKYP-NLQHVIDAVGSEDSIPEAYKVTADSLPATLL-----EVVPM
                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypotherical 41.6 kDa"protein in IMPI-HLJ1 intergenic region (RF1095).
YMR152W OR YM9375.22 OR YM8520.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91360060; PubMed-1886606;
Behrens M., Michaelis G., Pratje E.;
"Mitochondrial inner membrane protease 1 of Saccharomyces cerevisiae
shows sequence similarity to the Escherichia coli leader peptidase.";
Mol. Gen. Genet. 228:167-176(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G., "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotia; Saccharomycota; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0004760; YIMI.
GO; GO:0005811; Clipjd particle; IDA.
GO; GO:0005743; C:mitochondrial inner membrane; IDA.
GO; GO:0008233; P:peptidase activity; IMP.
GO; GO:0006627; P:mitochondrial processing; IMP.
InterPro; IPRO2085; Adh zn family.
PF00107; ADH_zinc_N; I.
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S -> I (IN REF. 1
D -> N (IN REF. 1
                                                                                                                                                                                                             332 GDIH-HMNIKVFSNGLDDVPALTEGIKEGKN 361
                                                                                                                                                                                                                                     | : :: || :: | | GOVKLFVDKKVF-HGLSSVADAVDHLYSGAN 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 387:90-93(1997).
-1- SIMILARITY: SOME, TO YEAST AST1/AST2.
                                                                                                                                                                                                                                                                                                                                                 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S55518; AAB19702.1; -. EMBL; Z47071; CAA87367.1; -. EMBL; Z49705; CAA89788.1; -. PIR; S50409; S50409.
                                                                                                                                                                                                                                                                                                                                               STANDARD;
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STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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PubMed=9169872;
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CONFLICT
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SEQUENCE FROM N.A.

MEDLINE=95107343; PubMed=7808470;

Liu X., Chang K.P.,

Liu X., Chang K.P.,

Identification by extrachromosomal amplification and overexpression
of a zeta-crystallin/NADPH-oxidoreductase homologue constitutively
of a zeta-crystallin/NADPH-oxidoreductase homologue constitutively
of a zeta-crystallin/NADPH-oxidoreductase homologue constitutively
Mol. Blochem. Parasitol. 66:201-210 (1994).
-!- CATALYTIC ACTIVITY: NADPH + quinone = NADP(+) + semiquinone.
-!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family. Quinone oxidoreductase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHINAYTKIVTVASKKHEKLLKSYGADDVPDYHDAGVIEQIKSKYPNLQHVIDAVGSEDS 250
                                                                                                                               251 IPEAYKVTADSLPATLLEVVPMTIESIPEBIRKDNVKIDITLLYRASGQEILLGATRFPA 310
                                                                                                                                                     55 GPEGSIL-----GCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAE 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania amazonensis.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5659;
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                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Lagt sequence update)
01-OCT-1996 (Rel. 34, Lagt annotation update)
Possible quinone oxidoreductase (RC 1.6.5.5) (NADPH:quinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 340;
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23.5%; Pred. No. 0.00051;
tive 58; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 AA
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InterPro; IPR002364; QOR zeta crystal.
                                                                                                                                                                                                           311 SPEYHEATVKFVKFINPHLNN 331
                                                                                                                                                                                                                                               255 EINPRDIMAKETSIIGVSLSS 275
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                                                                                                                                                                                                                                                                                                                                               STANDARD;
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P42865;
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WEDLINE-21016721; PubMed=11130714;

MEDLINE-21016721; PubMed=11130714;

MEDLINE-21016721; PubMed=11130714;

MAYAJima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,

MAYAZAZAKI N., Naruo K., Okumura S., Shingo S., Takeuchi C., Wada T.,

Makazaki N., Naruo K., Okumura S., Shingo S., Takeuchi C., Wada T.,

Matanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,

Matanabe A., Yamada M., Yasuda M., Solingo S., Takeuchi C., Wada T.,

Matanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,

Matanabe A., Yamada M., Yasuda M., Saton R.,

Babraman K., Murxay J., Johnson D., Rohlfing T., Nelson J.,

Belter B., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,

Belter B., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,

Belter B., Cordum H., Cordes M., Courtney E., Lamar E., Latreille P.,

Belter B., Myara M., Rodriguez M., Hoon See L., Vil D., Baker J.,

RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,

RA Parnell L., Shah R., Rodriguez M., Murphy G., Bancroft I.,

RA Volkaert G., Wambutt R., Wulson R.K., Murphy G., Bancroft I.,

RA Volkaert G., Wambutt R., Duesterhoeft A., Stiekem W., Pohl T.,

RA Battian K.-D., Terryn N., Hartley N., Bent E., Johnson S.,

Langham S.-A., McCullagh B., Ramsperger U., Wedler R., Wedler B., Peters S.,
                                                                                                                                                                                                            PKTYSRDYSGVIIKAGKDVDNRWKVGDKVNGMYSHIYG-----ERGTLTHYLILNPAKD 120
                                                                                                                                                                                                                                            -PLPYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHT 170
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                                                                                                                                                                                                                                                                                                           171 HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQ 230
                                                                                                                                                                                                                                                                                                                             58 GSILGCDIAGTVVXLGPNASTDLKVGDTGFGF---VHGASQTDPKNGAFAEYARVYP--- 111
                                                                                                                                 TNKSVIYVNNITPVIITSSELDLRSCYQDDEVVIEVHAAALNPIDFITHQLCNSYIFGKY 66
                                                                                                                 6 TQKAVIIEGDKAVVKTDVSVPELK----EGTALVKVEAVAGNPTDW-KH---1AYKIGPE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable NADP-dependent oxidoreductase FI (EC 1.....).
Pl OR AT5G16970 OR F2K13 120.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Columbia;
MEDLINE=96064691; PubMed=7592828;
Bablychuk E., Kushnir S., Belles-Boix E., van Montagu M., Inze D.;
"Arabidopsis thaliana NADPH oxidoreductase homologs confex tolerance
of yeasts toward the thiol-oxidizing drug diamide.";
J. Biol. Chem. 270:26224-26231(1995).
                                                                                 40;
                                                   Length 365;
                                                8.0%; Score 154; DB 1; Length 36
23.5%; Pred. No. 0.00066;
ive 49; Mismatches 116; Indels
L -> S (IN REF. 1).
88F6453D9E918A16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 AA
                                                                                                                                                                                                                                                                                                                                                                                           231 IKS-KYPNLQH-----VIDAVGSEDSIP 252
                  41637 MW;
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                  365 AA;
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
                                                                                 63;
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                  SEQUENCE
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                                                Query Match
   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 EYARVYPPLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 CSPKEGETVYVSAASGAVGQLAKMMGCYV-VGSAGSKEKVDLLKTKFGFDDAFNYK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TOKAVII-----EGDKAVVKTDVSVPELKEGT--ALVKVEAVAGNPTDWKHIAYKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 STPOHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKS-YGADDVFDY-
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                                             ŝ
                                                                                                                                                                                                                                                                        -!- FUNCTION: MAY PLAY A DISTINCT ROLE IN PLANT ANTIOXIDANT DEFENSE AND IS POSSIBLY INVOLVED IN NAD(P)/NAD(P)H HOMEOSTASIS.
-!- SIMILARITY: BELONGS TO THE L4BD FAMILY OF NADP-DEPENDENT OXIDOREDUCTASE.
van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel Peldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W., Bents O., Lemcke K., Kolesov G., Mayer K.F.x., Rudd S., Schoof H., Schueller C., Zaccaria P., Mewes H. W., Bevan M., Fransz P.F.; "Sequence and analysis of chromosome 5 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kluyveromyces marxianus (Yeast) (Kluyveromyces fragilis).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38134 MW; 5AFCEBB2948B2680 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Mismatches 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.0%; Score 153.5; DB 1
22.5%; Pred. No. 0.00066;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alcohol dehydrogenase 1 (EC 1.1.1.1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002085; Adh zn family. Pfam; PF00107; ADH zinc N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z49768; CAA89838.1; -. EMBL; AL391141; CAC01710.1; PIR; S57611; S57611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 22.59
Matches 91; Conservative
                                                                                                                                                                                                                                                                 Nature 408:823-826(2000)
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SEQUENCE 345 AA;
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ADH2 OR ADHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | | ::| : | K-LPLVGGHEG-----AGIVVAMGENV-TGWEIGDYAGIKWLNGSCMSCEECELSNEP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 -DPK-----NGAFAEYARVYPPLFYKSNLTHSTADEISEGPV-KNFESAASLPVSLT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 TAGVSLCHHLGSKM----EWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGDEKAKLFKELGG---------EYFIDFTKTKDMVAEVIEATNGVA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATLLEVVPMTIESIPEEIRKDNVKIDITLLY-RASGOEILLGATR-FPASPEYHEATVK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 HAVI------NVSVSEAAISTSVLYTRSNGTVVLVGLPRDAOCKSDVFNOVVK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVPTTQKAVII--EGDKAVVKTDVSVPELKEGTALVKVE------AVAGN-PTDW 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 KHIAYKIGPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFGFVHGASQT-----96
                                                                                                                                         SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                            binding; NAD; Multigene family.
ZINC 1 (CATALYTIC) (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMILARITY).
ZINC 1 (CATALYTIC) (BY SIMILARITY).
;, A75DZEBEB2E355BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.6%; Pred. No. 0.0006/;
tive 53; Mismatches 142; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 348;
                                                                                                                               COFACTOR: Binds 2 zinc ions per subunit (By similarity)
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
VCDI_TaxID=4911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVKFINPHLNNGDIHHMNIKVFSNGLDDVPALTEGIKE 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 153.5; DB 1
22.6%; Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                   PIR; SJ2341; SJ2341.
InterPro; IPR002328; ADH zinc.
InterPro; IPR002006; Adh zn family.
Pfam; PP00107; ADH zinc N; I.
PROSITE; PS00059; ADH ZINC; I.
Oxidoreductase; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                               ZINC 1
ZINC 2
ZINC 2
ZINC 2
ZINC 2
ZINC 2
                                           STRAIN=ATCC 12424;
MEDLINE=93250057; Pubmed=8485163;
                                                                                                                                                                                                                                                                                                                                                                                                                                            348 AA; 37158 MW;
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                                 SEQUENCE FROM N.A.
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                                                                                                                                                                          family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVPTTQKAVIIE--GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTD---WK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
-1- SUBUNIT: Homoterramer (By similarity).
-1- SUBCELLUIAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast 14:1311-1325(1998).
-!- FUNCTION: CONVERIS ETHANOL TO ACETALDEHYDE.
-!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone
                                                                                                                                                                                                                                                                                                                                                                            Cho J.Y., Jeffries T.W.; "Pichia stiplis genes for alcohol dehydrogenase with fermentative and respiratory functions.";
                                                                                                                                                                          Pichia stipitis (Yeast).
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
          ADMA_FALCSI
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alcohol dehydrogenase II (EC 1.1.1.1) (ADH 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                Appl. Environ. Microbiol. 64:1350-1358(1998)
[2]
  348 AA
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 58785 / CBS 6054;
MEDLINE=98207839; PubMed=9546172;
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CBS 5774;
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QOR BOVIN
097764;
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SEQUENCE
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Matches
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                SKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSLP 263
                                                                                                                                                                                         264 ATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLGATRFPA----SPEYHEATV 319
                                                                                                                                                                                                                                                             ATNGGAHGVINVSVSERAMQQSVD----YVRPTGTVVLVG---LPAGAKVSASVFSSVV 286
                                                       ------PKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPV-KNFESAASLPVSLTT 147
                                                                                  112 CPDADLSGYTHDGSFQQYA------TADAIQAARIPKGTDLALIAPI--LC 154
                                                                                                                AGVSLCHHLGSKM----EWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVA 203
                                                                                                                                            AGITVYKALKTAQLQAGQW------VAVSGAAGGLGSLAIQYAKAMGYRVVGIDGG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast 14:1311-1325(1998).
-1- FUNCTION: CONVERTS ETHANOL TO ACETALDEHYDE AND PLAYS A MAJOR ROLE
IN XYLOSE FERMENTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=99019018; PubMed=9802210; Paierstall T., Klinner U.; Passoth V., Schaefer B., Liebel B., Weierstall T., Klinner U.; Molecular cloning of alcohol dehydrogenase genes of the yeast Pichia stipitis and identification of the fermentative ADH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPACTOR: Binds 2 zinc ions per subunit (By similarity).
SUBUNT: Homotekramer (By similarity).
SUBCELLULAR LOCATION: Cytcoplasmic.
SUBCELLULAR LOCATION: Cytcoplasmic.
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with fermentative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
HIAYKIGPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFGFVHG-
                                                                                                                                                                                                                                                                                                           320 KFVKFINPHLNNGDIHHMNIKVFSNGLDDVPALTEGIKE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cho J.Y., Jeffries T.W.; "Pichia stipitis genes for alcohol dehydrogenase and respiratory functions.";
                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADH1 OR ADH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appl. Environ. Microbiol. 64:1350-1358(1998)
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                                                                                                                                                                                                                                                                                                                                                                                             348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 58785 / CBS 6054;
MEDLINE=98207839; PubMed=9546172;
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pichia stipitis (Yeast).
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000097;
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EMBL; AF008245; AAC49991.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 IAYKIGPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFGFVHGA-----SQTDPKNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPM 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 TIESIPEEIRKDNVKIDITLLYRASGQEILLGATRFPASPE----YHEATVKFVKFINPH 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ---SVSEKAIAQSCQ----YVRSTGTVVLVG---LPAGAKVVAPVPDAVVKSISIRGSY 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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-1- FUNCTION: DOES NOT HAVE QUINONE REDUCTASE ACTIVITY. BINDS STRONGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---WK-----H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AFAEYARVYPPLFYKSNLTH----STADBISEGPVKNFESAASLP--VSLTTAGVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 CAGITVYKALKTAQIQPGNWVCİSGAGGGLĞSLAIQYAKAM-GFRVİAIDGGEEKGEFVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 SLGAEAYVDF-----------TVSKDIVKDIQTAT-DGGPHAAINV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rao P.V., Gonzalez P., Persson B., JOETNVALL H., VELLAGIO, C., Zigler J.S. Jr., "Glinea pig and bovine zeta-crystallins have distinct functional characteristics highlighting replacements in otherwise similar
                                                                                                                                                                                                    SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 348;
                                                                                                                                                                 NAD; Multigene family.
(CATALYTIC) (BY SIMILAR
(CATALYTIC) (BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSVPTTOKAVIIEGDKA-VVKTDVSVPELKEGTALVKVEAVAGNPTD-
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                                                                                                                                                                                                                                                                       (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(CATALYTIC) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 149.5;
InterPro; IPR002328; ADH zinc.
InterPro; IPR002085; Adh zinc, Femily.
Prom; Pro10107; ADH zinc N; I.
PROSTITE; PR00107; ADH ZINC N; I.
Oxidoreductase; Zinc; Metal-binding; NA:
METAL 44 ZINC; I.CA
METAL 98 98 ZINC I (CA
METAL 101 101 ZINC 2 (BY
METAL 112 112 ZINC 2 (BY
METAL 112 112 ZINC 2 (BY
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36520 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 23.6%;
nes 92, Conservative 5
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                                                                                                                                                                                                                                                                                                                                                          104
112
154
348 AA;
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HSSP; P28304; 100R
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLDFKQGAAIGIPYFTAYRALLYSA-----PVKPGES--VLVHGASGGVGIAACQIAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 HINAY-TKIV-TVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSED 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --AYGLKVLGTASTEEGQKIVLENGAHKVFNHKEANYIDKIKK-----SVGEKG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GESVSA-FKKGDRVF-----TTRTISGGYAEYALAADHTVYTL-------PE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LQSDVAVPIPKDHQVLIKVQACGVNPVDTYIRSGTHNIKP---LLPYTPGFDVAGIIEAV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 VKTDVSVPELKEGTALVKVEAVAGNPTDW--KHIAYKIGPEGSIL----GCDIAGTVVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLGA 305
                   SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Lama.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB-Lens;

BELIXRE-96073447; PubMed=7476124;

Gonzalez P., Rao P.V., Nunez S.B., Zigler J.S. Jr.;

Gonzalez P., Rao P.V., Nunez S.B., Zigler J.S. Jr.;

"Evidence for independent recruitment of zeta-crystallin/quinone reductase (CRYZ) as a crystallin in camelids and hystricomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 AA; 35403 MW; BD24ACD857BA8673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.7%; Score 148; DB 1; Best Local Similarity 24.0%; Pred. No. 0.0016; Matches 71; Conservative 54; Mismatches 9:
                                                                                           family. Quinone oxidoreductase subfamily.
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InterPro; IPR002085; Adh_zn_family.
InterPro; IPR002564; QOR_zeta_crystal.
                                                                                                                                                                                                                                                                                                                                                                                                                        PFOSITE; PS01162; OOR ZETA CRYSTAL; 1.
                                                                                                                                                                                                                                                                                                                                 EMBL; U70048; AAD10290.1; -.
    SINGLE-STRANDED DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lama guanicoe (Guanaco)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinc; DNA-binding.
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Q28452;
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AC 0284 I

DT 15-JU

DT 15-JU

DT 15-JU

DE 01105

GN CRYZ.

GN LAMM

CRYZ.

OC BUKAR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 ASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 ESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 LQSDVAVPIPEEHQVLIKVQACGVNPVDTYIRSGTYSRKPRLPYTPGLDVAGLIBAVGBR 83
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable NADP-dependent oxidoreductase P2 (EC 1.-..-).
P2 OR ATSG16990 OR PZK13_140.
Arabidopsis thalians (Nousean cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida II; Brassicales; Brassicacese; Arabidopsis.
                                                   DETOXIFICATION OF XENOBIOTICS (BY SIMILARITY).

CATALYTIC ACTIVITY: NADPH + quinone = NADP(+) + semiquinone.
SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase family. Quinone oxidoreductase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia, MEDLINE=96064691; PubMed=7592828; Bablychuk E., Kushnir S., Bellee-Boix E., van Montagu M., Inze D.; "Arabidopsis thaliana NADPH oxidoreductase homologs confer tolerance of yeasts toward the thiol-oxidizing drug diamide."; J. Biol. Chem. 270;26224-26231(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------IDVIIEMLANVNLSNDLNLLSQ-GGRVIIVGS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 330;
ORTHOQUINONES ARE THE BEST SUBSTRATES. MAY ACT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.7%; Score 148; DB 1; Length 33
23.1%; Pred. No. 0.0016;
tive 51; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 AA; 35187 MW; E784E414D2BA23D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002085; Adh zn family.
Interpro; IPR002364; QOR_zefa_crystal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00107; ADH zinc N; 1. PROSITE; PS01162; QOR ZETA CRYSTAL; 1. Oxidoreductase; NADP; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L34159; AAA99986.1; -.
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EYARVYPPLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHP 164
                                                                                                                                                                                                                                                                                                                          ----GPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFGFVHGASQTDPKNGAFAEYARV 109
                                                                                                                                  106 BYSVITPMAHMHPKIQH-----TDVPLSYYTGLLGMPGMTAYAGF-----YEV
                                                                                                                                                                                                    223 HDAGVIEQIKSKYP-NLOHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEI
                                                                                                                                                                                                                                                                                               282 RKDNVKIDITLLYRASGQE-----ILLGATRFP--ASPEYHEATVKFVKFINPHLNNG
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                                                                                                         165 STPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKS-YGADDVFDY-
                                                                                                                                                                                                                               208 EESDLSAALKRCFPKGIDMYFENVGGK------MLDAVLLMMVPHGRIAVCGMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBUNIT: Homotetramer.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90273773; PubMed=2190430;
Saliola M., Shuster J.R., Falcone C.;
"The alcohol dehydrogenase system in the yeast, Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D71BE2D5CC86119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        | : :: ::||: | |: || | |: || | 306 KITY--VEDVADGLEKAPEALVGLFHGKNVGKQVVVIAR 342
                                                                                                                                                                                                                                                                                                                                                                                             333 DIHHMNIKVFSNGLDDVPALTEGIKEGKN--KNVKYVAR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 145.5; DB 1;
; Pred. No. 0.0025;
49; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alcohol dehydrogenase I (EC 1.1.1.1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%;
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Best Local Similarity 23.09
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6:193-204 (1990)
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P20369;
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MEDLINE-21016721; PubMed=11130714;

MEDLINE-21016721; PubMed=11130714;

MEDLINE-21016721; PubMed=11130714;

MEDLINE-21016721; PubMed=11130714;

MEDLINE-21016721; PubMed=11130714;

MARAZAKI N., Naruo K., Okumura T., Hosouchi T., Kawashian K.,

MARAZAKI N., Naruo K., Okumura S., Shingo S., Takeuchi C., Wada T.,

MARAZAKI N., Naruo K., Okumura S., Shingo S., Takeuchi C., Wada T.,

MADERMANN K., Murray J., Johnson D., Rohling T., Nelson N.,

Abermann K., Murray J., Johnson D., Rohling T., Nelson J.,

Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,

Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,

Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,

Belter E., Cordum H., Sakhar B., Martenile P.,

Belter E., Cordum H., Scheth M., Belt M., Dedhia N.,

Belter E., Cordum H., Roher B., Otersky P., Riley A., Strowmatt C.,

Namer M., Mayer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,

Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,

Antienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,

Nolckaert G., Wambutt R., Duesterhoeft A., Stickems M., Pohl T.,

Antiens S. A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,

Meltzenegger U., Wedler H., Balke K., Wedler B., Petrers S., Hempel S.,

Meltzenegger U., Wedler H., Balke K., Wedler B., Patarse V.,

Meltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

Ramsperger U., Wedler H., Salke K., Wedler B., Petrers S.,

Meltzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

Reldpausch M., Lamberth S., Willarroel R., Gielen J., Ardiles W.,

Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P. F.,

"Heldpausch M., Bent B., Mewes H.-W., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bernei S., Schoof H.,

"Heldpausch M., Bente B., Mewes H.-W., Bevan M., Weller B., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Bevan M., Meller B., Belter B., Belter B., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstantion the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 TDWKHIAYKIGPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFA 104
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21.6%; Pred. No. 0.0023;
tive 61; Mismatches 160; Indels
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491698EF58BA82DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMEL; AL391141; CAC01712.1; --
EMEL; AV091220; AAM14259.1; --
EMEL; AV065253; AAL38729.1; --
FIR; S57612; S57612.
FIR; T1554; T51554.
INTEPTO; IPRO2085; Adh zn family.
Fram; PRO0107; ABH zinc_N; T.
Oxidoreductase; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 AA; 37989 MW;
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86; Conservative
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or send an email to license@isb-sib.ch)
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350 AA;
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NCBI_TaxID=53953;
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Matches
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       SO STITITION SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOLVER SOL
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64 PLVGGHEG------GGVVVAMGENVK-GWKIGDFAGIKWLNGSCMS------CEYCEL 108
                                                                                                                                                                                                                                                                                         110 YP----PLFYKSNLTH-----STADEISEGPVKNFESAASLPVS-----LTTAGV 150
                                                                                                                 SNESNCPEADLSGYTHDGSFQQYATADAV-----QAAKIPVGTDLAEVAPVLCAGV 159
                                                                                                                                                                SLCHHLGSKM----EMHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKK 206
                                                                                                                                                                                                                                                                                                                                                   265 TLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLGATR-FPASPEYHEATVKFVK 323
                                                                                                                                                                                                                                                                                                                                                                                                 -----TNYVRSNGTVVLVGLPRDAKCKSDVFNOVVKSIS 292
                                                                                                                                                                                                                                                       207 HEKLLKSYGADDVFDYHDAGVI--EQIKSKYPNLQHVIDAVGSEDSIPEAYKVTADSLPA 264
                                                                                                                                                                                               160 TVYKALKSANLKAGDW------VAISGAAGGIGSLAVQYAKAM-GYRVLGIDAGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: Binds 2 zinc ions per subunit (By similarity).
SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJNE-96287648; PubMed-8686375; Bertram G., Swoboda R.K., Gooday G.W., Gow N.A.R., Brown A.J.P.; Bertram G., Swoboda R.K., Gooday G.W., Gow N.A.R., Brown A.J.P.; "Structure and regulation of the Candida albicans ADH1 gene encoding an immunogenic alcohol dehydrogenase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alcohol dehydrogenase 1 (EC 1.1.1.1) (40 kDa allergen) (Allergen
Can a 1) (Can a I).
Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida. (COTI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92136159; Pubmed=1777830;
Shen H.D., Choo K.B., Lee H.H., Haleh J.C., Lin W.L., Lee W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Exp. Allergy 21:675-681(1991).
-!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pendrak M.L., Klotz S.A., Smith R.L.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                             324 FINPHLANGDIHHMAIKVFSNGLDDVPALTEGIKE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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01-NOV-1995 (
15-SEP-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 GEADLSGYTHDGSFEQYA------TADAV-----QAAKIPAGTDLAN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 VS--LCHHLG-----SKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 KIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 VAIDGGDEKGE-FVKSLGABAYVDF--------TKDKDIVBAVKK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 TADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLY-RASGOBILLGATRPPA----S 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 I----GPEGSILGCDIAGTVVKLGPNASTDLKVGD-TGFGFVHGASQT-----DPK- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEYHEATVKFVKFINPHLNNGDIHHMNIKVFSN------GLDDVPALTEGIKEGK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S IPKTQKAVVFDTNGGQLVYK-DYPVPTPKPNELLIHVKYSGVCHTDLHARKGDWP-LATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 VPTTQKAVIIE--GDKAVVKTDVSVPELKEGTALVKVE-----AVAGNPTDWKHIAYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                             1-binding; NAD; Allergen.

ZINC 1 (CATALYTIC) (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

ZINC 1 (CATALYTIC) (BY SIMILARITY).

ZINC 1 (CATALYTIC) (BY SIMILARITY).

R -> N (IN REF. 2).

R -> T (IN REF. 2).

R -> A (IN REF. 2).

D -> A (IN REF. 3).

C -> L (IN REF. 3).

D -> B (IN REF. 3).

D -> B (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.0035;
57; Mismatches 123; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C3DFE2E70F42D634 CRC64;
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15-SEP-2003 (Rel. 42, Lact sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable L-threonine 3-dehydrogenase (EC 1.1.1.103)
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                                              PIR; S63781; S52153.

COMPLUYEAST-2DPAGE; P43067; -.
InterPro; IPR002328; ADH zinc.
InterPro; IPR002085; Adh zn family.
Ffam; PF00107; ADH zinc N; I.
PROSITE; PS00059; ADH ZINC; I.
Oxidoreductase; Zinc; Metal-binding; NR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36879 MW;
EMBL; X81694; CAA57342.1; -. EMBL; U15924; AAA53300.1; -.
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tes 94; Conservative
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GEVVGIGQEVK-GFKIGDRVSGEGHITCGHCRNCRGGRTHLCRNTIGVGVNRP--ĠCFÀÈ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=06:HI / CFT073 / ATCC 700928;
MEDLINE=2238224; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.: Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
-1- PATHWAY: Threonine catabolism; first step.
-1- SUBUNIT: Homoterramer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches 147; Indels 118; Gaps
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AAB2927DC7801C1E CRC64;
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Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
CATALYTIC ACTIVITY: L-threonine + NAD(+) = L-2-amino-3-oxobutanoate + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 341;
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                                                                                                                                                                                                           15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
L-threonine 3-denydrogenase (EC 1.1.1.103).
                                                                                  341 AA
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InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn family.
InterPro; IPR002055; Adh_zn family.
InterPro; IPR004627; Tdh.
Pfam; PF00107; ADH_zinc N; 1.
TIGRFAMS; TIGR00695; ADH_Zinc, 1.
PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductase; NAD; Zinc; Metal-bindi
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                                                                                  STANDARD;
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R PRSP; H71110; H711...

R RSSP P25984; 1KEV.

DR HAMAP; MF 00627; -; 1.

DR InterPro; 1PR002328; Adh_zn_family.

DR InterPro; 1PR002328; Adh_zn_family.

DR PROSTE; P500059; Adh_zn_family.

DR PROSTE; P500059; Adh_zn_family.

DR PROSTE; P500059; Adh_zn_family.

DR PROSTE; P500059; Adh_zn_family.

DR TIGRPAMs; TIGRO059; Adh_zn_c family.

DR PROSTE; P500059; Adh_zn_c family.

DR PROSTE; P500059; Adh_zn_c family.

DR TIGRPAMs; TIGRO069; Adh_zn_c family.

DR PROSTE; P500059; Adh_zn_c family.

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                                                            MEDLINE-98344137; PubMed=9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxobutanoate + NADH.

COFACTOR: Binds 2 zinc ions per subunit (By similarity).

PATHWAY: Threonine catabolism; first step.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 5:55-76(1998).
-!- CATALYTIC ACTIVITY: L-threonine + NAD(+) = L-2-amino-3-
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SEQUENCE FROM N.A.
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                                          222
                                                   YARVYPPLFYKSNLTHSTADEISE--GPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWH 163
                                                                                                                     LLEVVPMTIESIPEEIRKDNVKIDIT-LLYRASGQEILLGATRFPASPEYHEATVKFVKF 324
                                                                                                                                  BE
             YLVI--PAFNAFKIPDNISDDLASIFDP---FGNAVHTALSFDLVGED------
                                      164 PSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDY-
                                                                               ----HDAGVIEQIKSKYPNLQHVIDAVGSEDSI-----PEAYKVTADSL----PAT
                                                                                                201 LELARKMGITRAVNVAKENLNDVMTELGMTEGFDVGLEMSGAPPAFRTMLDTMNHGGRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NCA 1503;
MEDLINE=92138636;
Sakoda H., Imanaka T.,
"Cloning and sequencing of the gene coding for alcohol dehydrogenase of Bacillus stearothermophilus and rational shift of the optimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: Binds 2 zinc ions per subunit (By similarity).
ENZYME REGULATION: SUBSTRATE INHIBITION IS NOT OBSERVED WITH ANY
A LACOHOLS, AND THE ENZYME-NADH DISSOCIATION IS NOT CONSIDERED TO E
A RATE-LIMITING STEP.
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=79169263; PubMed=436831;
Jeck R., Woenckhaus C., Harris J.I., Runswick M.J.;
"Identification of the amino acid residue modified in Bacillus
strearchermophilus alcohol dehydrogenase by the NAD+ analogue 4-(3-
bromoacetylpyridinio)buryldiphosphoadenosine.";
Eur. J. Biochem. 93:57-64(1979).
                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCDI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-45.
MEDLINE-73229257; PubMed-4578954;
Bridgen J., Kolb E., Harris J.I.;
"Amino acid sequence homology in alcohol dehydrogenase.";
                                                                                                                                                                         325 INPHLNNGDI -- HHMNIKVFSNGLDDVPALTEGIKEGK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-37; 188-197; 247-263 AND 324-336
                                                                                                                                                                                                                                             (Rel. 12, Created)
(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND MUTAGENESIS.
                                                                                                                                                                                                                                                                         15-SEP-2003 (Rel. 42, Last annotation
Alcohol dehydrogenase (EC 1.1.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 174:1397-1402(1992)
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 33:1-3(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 34-54.
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01-NOV-1995
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P12311;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 VFDYHDAGVIEQIKSKYPNLOHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIP 278
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ZINC 1 (CATALYTIC) (BY SIMILARITY).
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ZINC 1 (CATALYTIC) (BY SIMILARITY).
T-SS. LITTLE DECREASE IN ACTIVITY.
T-SS. LITTLE DECREASE IN ACTIVITY.
T-SN IN ACTIVITY.
T-SN NO ACTIVITY.
H-SA: NO ACTIVITY.
MISSING (IN REF. 2).
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MISSING (IN REF. 2).
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InterPro; IPR002329; ADH zinc.
InterPro; IPR002035; Adh zin Emily.
PEam; PF00107; ADH zinc N; I.
PROSITE; PS00059; ADH ZINC; I.
Oxidoreductage; Zinc; Metal-binding;
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337 AA;
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CONFLICT
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R PR; G75649; G7552.

R RSSP, P25984; IKEV.

DR HAMAP; MF_00627; -; 1.

DR InterPro; IPR002583; Adh_zn_family.

DR InterPro; IPR002583; Adh_zn_family.

DR PGEM; PF00107; ADH zinc. N; 1.

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                                                                                                                                                                                                                                                                              Cohen GN., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O. Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; archaeon Pyrococcus abyssi."; Mol. Microbiol. 471495-1512(2003).

-!- CATALYTIC ACTIVITY: L-threonine + NAD(+) = L-2-amino-3-oxobutanoate + NADH.

-!- COPACTOR: Binds 2 zinc ions per subunit (By similarity).

-!- PATHWAY: Threonine catabolism; first step.
-!- PATHWAY: Threonine catabolism; first step.
-!- SIBELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIBELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                       Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
bable L-threonine 3-dehydrogenase (EC 1.1.1.103) OR PYRAB13870 OR PAB2382.
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PubMed=12622808;
                                                                                                                                                                                                         FROM N.A.
                                                                                                                                             NCBI_TaxID=29292;
                                                               Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-0157:H7 / RIMD 0509952;

MBDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxobutanoate + NADH.
-!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
-!- PATHWAY: Threonine catabolism; first step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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PROSITE; PS00059; ADH ZINC; 1.

Oxidoreductase; NAD; Zinc; Matal-binding; Complete proteome.

METAL 83 83 ZINC 1 (CATALYTIC) (BY SIMILARITY).

METAL 63 63 ZINC 1 (CATALYTIC) (BY SIMILARITY).

METAL 93 93 ZINC 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bscherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                             Q8XEJ1;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
L-threonine 3-dehydrogenase (EC 1.1.1.103).
TDH OR Z5043 OR ECS4494.
                                                                                                                                                                                                                                  341 AA.
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HAMAP; MF_00627; -; 1.

InterPro; IPR002238; AbH zinc.

InterPro; IPR002085; Adh_zn family.

InterPro; IPR004627; Tdh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacterlaceae, Escherichia.
NCBI_TaxID=83334;
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TIGRFAMS; TIGR00692; tdh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:529-533(2001).
                                                                                                                                                                                                                              STANDARD;
: |::::
220 FEEDVVKEV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                               Zinc, Metal-binding.
8 ZINC 1 (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                           (CATALYTIC)
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ZINC 2
ZINC 2
ZINC 2
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ZINC 2
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6-OCT-2001 (Rel. 40, Last seq
5-SEP-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                         EMBL; AE015373; AAN45103.1; -.
                                                                                                                                                                                                                                                                                     HAMAP; MF_00627; -; 1.
PROSITE; PS00059; ADH_ZINC; 1.
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37255 I
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63
93
96
107
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METAL 38 3
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124 YLVI--PAFNAFKIPDNISDDLASIFDP---FGNAVHTALSFDLVGED------ 166
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-! CATALYTIC ACTIVITY: L-threonine + NAD(+) = L-2-amino-3-Oxobutanoate + NADH.

-! COFACTOR: Binds 2 zinc ions per subunit (By similarity).

-! PATHWAY: Threonine catabolism; first step.

-! SUBUNIT: Homotetramer (By similarity).

-! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang P., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
   ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (GATALYTIC) (BY SIMILARITY).
T -> N (IN REF. 2).
                                                                                                                                                                                                                                                         118;
                                                                                                                                                                                            DB 1; Length 341;
                                                                                                                                                                                  7.3%; Score 141; DB 1; Length 341
80.4%; Pred. No. 0.0052;
Ive 52; Mismatches 147; Indels
99 99 ZINC 2 (BY SIMILARITY).
107 107 ZINC 2 (BY SIMILARITY).
148 148 ZINC 1 (CATALYTIC) (BY SIN
54 54 T -> N (IN REF. 2).
341 AA; 37202 MW; AAB2877DDD5FACIE CRC64;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation.update)
1-threonine 3-dehydrogenase (EC 1.1.1.103).
TDH OR SF3656.
                                                                                                                                                                                                                                                                                                                                                                                                                                     GTVVKLGPNASTDLKVGDTGFGFVH-----
                                                                                                                                                                                                                     20.4%;
                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                  Local Similarity
les 81; Conserv
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Shigella flexneri
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P59409;
                                                            METAL
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GASQTDPKNGAFAE 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 IEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTD-----WKHIAYKIGPEGSILGCDIA 66
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Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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MEDLINE-2043119; PubMed=10974568;
Ladriere J.-M., Georis I., Guerineau M., Vandenhaute J.;
"Kluyveromyces marxianus exhibits an ancestral Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.3%; Score 141; DB 1; Length 341; 20.4%; Pred. No. 0.0052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PLVGGHEG-----AGVVVAMGDNVK-GWKIGDLAGIKWLNGSCMNCEECELSNESNCP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NGAFAEYARVYPPLFYKSNLTHSTADEISEGPVKNFESAASLPVS---- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 DADLSGYTHDGSFQQYA-----TADAV-----QAAHIPAGTDLAQV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 --LITAGVSLCHHLGSKM----EWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 IVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVIDAVGSEDSIPEAYKVT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 ADSLPATL-LEVVPMTIESIPEEIRKDNVKIDITLLYRASGQEILLGATR-FPASPEYHE 316
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                                                                   COFACTOR: Binds 2 zinc ions per subunit (By similarity).
SUBUNIT: Homoctramer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                               CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVKFVKFINPHL-NNGDIHH------MNIKVFSNGLDDVPALTEGIKEGK 360
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AGETVATION (BY SIMILARITY).

ZINC 1 (CATALYTIC) (BY SIMILARITY).

ZINC 2 (BY SIMILARITY).

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54; Mismatches 138; Indels 133;
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                                                                                                                                                                                                                                                                                                                                                                           Pfan, PF00107; ADH zinc N; I.
PROSITE; PS00059; ADH ZINC; 1.
Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family;
 cerevisiae genome organization downstream of ADH2.";
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InterPro; IPR002085; Adh_zn family.
PFam: PF00107; ADH zinc_N; I.
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89; Conservative
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111
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347 AA;
                  255:83-91 (2000)
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INIT MET
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                                                                                                                                           family.
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MG1655,
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Bscherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
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                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Oxidoreductase; Zinc; Metal-binding; Manganese; Cobalt; NAD;
                                                                                                                                                                 Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.; "The primary structure of Escherichia coli L-threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CATALYTIC).
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                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-20 AND 149-153
01-AUG-1988 (Rel. 08, Created)
01-FRE1-191 (Rel. 17, Last sequence update)
12.5EP-2003 (Rel. 42, Last annotation update)
L-threonine 3-dehydrogenase (RC 1.1.1.103).
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ZINC 1
ZINC 2
ZINC 2
ZINC 2
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InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
InterPro; IPR000205; NAD_binding.
InterPro; IPR004627; Tdh.
                                                                                                                                                                                                     J. Biol. Chem. 264:5226-5232(1989)
                                                                                                                                                    MEDLINE=89174812; PubMed=2647748;
                                                                                       Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A33276; DEECTH.
ECO2DBASE; G038.8; 6TH EDITION.
EcoGene; EG10993; tdh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00107; ADH zinc N; 1.
TIGRFAMB; TIGR00692; tdh; 1.
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                                                              Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 RVYPPLFYKSNLTHSTADEISE--GPVKN-PESAASL-----PV8LTTAG-----VSLC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 HHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHBKLLKS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 RHVGAR------HVVI----TDVNBYRLELARKMGA-TRAVNVAQENLKDVMKE 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 TIESIP-EEIRKDNVKIDITLLYRASGQEILLGATRPPASPEYHEATVKPVKPINPHLNN 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 IEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTD-----WKHIAYKIGPEGSILGCDIA 66
                                                                                                                                                                     LKAEKGIWLVDAPKPEMGHNDLLIKIKKTAICGTDMHIYNWDEWSOKTIPVPMVVGHEYV
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Synaptic vesicle membrane protein VAT-1.
Torpedo californica (Pacific electric ray).
Bukaryota, Metazoa, Chondata, Cranlata; Vertebrata, Chondrichthyes;
Elasmobranchii; Squales, Hypnosqualea; Pristiorajes, Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
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ZINC 1 (CATALYTIC) (BY SIMI
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ZINC 1 (CATALYTIC) (BY SIMI.
W, 5378A4501153C7BF CRC64;
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                                                                                                                                                             EMBL; AE015899; AAN57632.1; -.
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96
107
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                                                                                                                                                                                                                                                                                                                                                                                   166 TPQHTHPLLIWGGATAVGQQLIQVAXHINAYTKIVTVASKKHEKLLKSYGADDVFDY--- 222
                                                                                                                                        12 IEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTD-----WKHIAYKIGPEGSILGCDIA 66
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                                                                                                                                                                 --HDAGVIEQIKSKYPNLQHVIDAVGSEDSI------PEAYKVTADSL----PATLL
                                                                                                  Gaрв
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-!- CATALYTIC ACTIVITY: L-threonine + NAD(+) = L-2-amino-3-
oxobuteanoate + NADH.
-!- COFACTOR: BAIMS 2 zainc ions per subunit (By similarity).
-!- PATHWAY: Threonine catebolism; first step.
-!- PATHWAY: Threonine catebolism; first step.
-!- SUBUNIT: Homoterzamer (By similarity).
-!- SUBCELULIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heidelberg J.F., Pauleen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Taspin A., Scott J., Beanan M., Erinkac L., Daudherty S., Madupu R., Todson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Vamathevan J., Neterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Kolonay J.F., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Genthence sequence of the dissimilatory metal ion-reducing bacterium
  ZINC 1 (CATALYTIC) (BY SIMILARITY). 039FBD6B1CE9C2B2 CRC64;
                                                        7.3%; Score 140; DB 1; Length 341;
20.2%; Pred. No. 0.0061;
:ive 52; Mismatches 150; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
L-threonine 3-dehydrogenase (EC 1.1.1.103).
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MEDLINE=22297686; PubMed=12368813;
                  341 AA; 37239 MW;
                                                                                                  Conservative
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Matches 80; Conserv
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63 CDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTHS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 GQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYP-NLQHV 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGATRFPASPE-----YHEATVKFVKFINP-----HLNNGDIHHMNIKVFSN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 LYGSANQVTAPKRSSLAAAKVWWHKFNIDALQLINSNKAVCGFHLGRTDPDHV----- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AVIIEG-----DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIGPEGS--ILG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AIVLNGVGGYDKVKVEVKKGVPTLKSDEILVRVQACGLNFSD---LLVRQGAFGKHHSLG 85
                                                                                                                  7.3%; Score 140; DB 1; Length 379;
22.8%; Pred. No. 0.007;
tive 51; Mismatches 139; Indels 102; Gaps
                                                                                                                                                                                                                                                            28 MOLECULES OF VAT-1.
SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY: QUINONE OXIDOREDUCTASE SUBFAMILY. STRONG, TO MAMMALIAN VAT-1 HOMOLOGS.
                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Electric lobe;
MEDLINE=90165593; PubMed=2483112;
Linial M., Miller K., Scheller R.H.;
"VAT-1: an abundant membrane protein from Torpedo cholinergic
                                                                                                                                                                                                                                                                                                                   PIR; JN0013; JN0013. InterPro; IPR002085; Adh_zn_family. InterPro; IPR002085; Adh_zn_family. InterPro; IPR002364; QOR_zeta_crystal. Pfam; PF00107; ADH_zinc_\overline{N}; 1. Crystal. PR001162; \overline{Q}OR_ZETA_CRYSTAL; 1. Oxidoreductase; \overline{Q}OR_ZETA_CRYSTAL; 1. Oxidoreductase; \overline{Z}OR_ZETA_CRYSTAL; 1. Oxidoreductase; \overline{Z}OR_ZETA_CRYSTAL; 1. Oxidoreductase; \overline{Z}OR_ZETA_CRYSTAL; 1. SEQÜENCE 379 AA; 41593 MW: FAAANNITECTION.
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Best Local Similarity 22.8*
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                            71;
                                                                                                                                                                                                                                                                                                                                        DB 3; Length 348;
                                                                                                                                                                                                                                                                                                                                                            49; Mismatches 160; Indels
                                                                                                                                                                                                                                                Harris D., Wood V., Rajandream M.A., Barrell B.G.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; All6531; CAB83005.1; -.. GeneDB SPombe; SPAC2E1P3.01; -.. InterPro; IPR002085; Adh. zn. family. Pfounty: abd. zinc; 1. EMD107; and zinc; 1. EMD107; and zinc; 1. EMD107; and zinc; 1.
                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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                                ALIGNMENTS
                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Rosales, Rosaceae, Rosoideae, Fragaria.
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EMBL; AB072893; BAC20562.1; -- SEQUENCE 362 AA; 39600 MW; CDB2CC5EFBED0E0F CRC64;
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                   Abe Y., Suzuki T., Ono C., Iwamoto K., Hosobuchi M., Yoshikawa H.; "Molecular cloning and characterization of an ML-236B (compactin) biosynthetic gene cluster in Penicillium citrinum.";
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MEDILINE-222227337; PubMed=12242508;
AADE Y., Suzuki T., Mizuno T., Ono C., Iwamoto K., Hosobuchi M. Yoshikawa H.;
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15.3%; Score 294; DB 3; Length 36
Best Local Similarity 26.9%; Pred. No. 2.8e-14;
Matches 104; Conservative 66; Mismatches 160; Indels
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STRAIN=cv. Chandler;
Lopez-Raez J.A., Redondo-Nevado J., Medina-Escobar N.,
Caballero-Repullo J.L., Munoz-Blanco J.;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
11-DR-2002 (TrEMBLrel. 20, Last annotation update)
Putative quinone oxidoreductase (Fragment).
Fragaria ananassa (Strawberry).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Genet. Genomics 267:636-646(2002)
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MEDLINE=22162865; PubMed=12172803;
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                                                                                                                                   NCBI_TaxID=5077;
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137 -----TAADERVLAHKP-KNLSFIEAASLPLAIETAHEGLERAELSAGK----- 179
                                                                                                                                                                                      166 TPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDA 225
                                                                                                                                                                                                                                                                                            226 GVIEQIKSKYPNLQHVIDAVGSEDSIPEAYK-----VTADSLPATLLEVVP---MTIE 275
                                                                                                                                                                                                                                                                                                                            234 N-FEDLPEKP---DVVYDAVGETDKAVKACKGCKVVTIVGPATPPAILFVLTSKGSVLE 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus terreus.
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=33178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kennedy J., Auclair K., Kendrew S.G., Park C., Vederas J.C.,
Hutchinson C.R.;
"Accessory Proteins Modulate Polyketide Synthase Activity During
Lovastatin Biosynthesis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                          13.9%; Score 266.5; DB 3; Length 26.3%; Pred. No. 3.6e-12; ive 69; Mismatches 156; Indels
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InterPro; IPR002085; Adh zn_femily.
Bern; PF00107; adh zinc; 1.
SEQUENCE 363 AA; 39511 WW; PDB9524DDB255713 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2001 (TrEMBLrel. 18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 PLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTA--GVSLCHHLGSKMEWHPSTPQH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 THPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIE 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 QIKSKYPNLQH----VIDAVGSEDSIPEAYK-----VTADSLPATLLEVVP---MTIE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 KIGPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDP-KNGAFAEYARVYP 111
                                                                                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                         SVPTTQKA-VIIEGDKA--WVKTD--VSVPELKEGTALVKVEAVAGNPTDWKH-IAY---
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DRC-2010 (TrEMBLrel. 19, Last annotation update)
Ripening-induced protein (Fragment).
Fragaria vesca (Woodland strawberry).
Fragaria visca (Woodland strawberry).
Spermatophyta; Manollophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Rosales; Rosaceae; Rosoldeae, Fragaria.
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     putative strawberry quinone oxidoreductase fruit ripening induced
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STRAIN-cv. Reine des Vallees;

Nam Y.W., Tichit L., Marty I., Lelievre J.M.;

"Isolation and characterization of cDNAs from genes differentially
"Isolation and characterization of submit of companies vesca L.).";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ001445; CAA04767.1;

InterPro; IPR002085; Adh_zn_family.
                                                                                                                                                                                                                                                                                         75;
                                                                                                                                                                                                                                      DB 10; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%; Score 277.5; DB 10; Length 29.7%; Pred. No. 4.6e-13; ive 52; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 SIPEEIRKDNVK--IDITLLY-------RASGQEIL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.1%; Score 271; DB 10; Length 3 30.5%; Pred. No. 1.4e-12; tive 50; Mismatches 113; Indels
"A putative strawbelly will protein.";

protein.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY048861; AAL06644.1; -.
InterPro; IPR002085; Adh_zn_family.
Pfan; PF00107; adh_zinc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                           Best Local Similarity 29.79
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 30.53
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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023939
1023939
AC 023939
DT 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD 01-DD
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Best Local Similarity 32.2%;
Matches 88; Conservative
 PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker J.R.;
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                   0945P3
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Q92E39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 THSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLY-RASG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDFKNGAFAEYARVYPPLFYKSNL 119
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A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
A Baqueror F., Berche P., Bloecker H., Brand P., Chakraborty T.,
Charbit A., Chercuani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Entian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
A Gautier L., Goebel W., Gomez-Lopez N., Hauf J., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
A Nordaisk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
T. Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KAVVIENYGGKEELKEKEVAMPKAGKNQVIVKEAATSINPIDWKLREGYLKOMMDWEPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 VVFDIMGGQIE-TDSYDVLKEG-TGRLVSIV----GISNEDRAKEKNVTATGIPHLQPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAVIIE---GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWK----HIAYKIGPE-GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::
EQLKELGKLLANKTIKPIVGAT-FPFSEKGVFDAHALSETHHAVGKIVISFN 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     b; Score 264; DB 16; Length 313;b; Pred. No. 4.4e-12;56; Mismatches 120; Indels 7.
                                                                                                                                                                                                                                                                Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294:849-852(2001).

EMBL, AL591976, CAC98691.1; -
ListList, LawO00613; -
InterPro; IPR002085; Adb_zn_family.

Pfam, PF00107; adb_zinc; 1.

Hypochetical protein; Complete protecome.

SEQUENCE 313 AA; 33940 MW; 0F1012C59A23621D CRC64;
                                                                                                                                                                        (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                      330 RVVQGGFDHIKQGMELVRKGELSGEKLVVRL 360
                   340 KVFSNGLDDVPALTEGIKEGKNKNVKYVARL 370
                                                                                                                                           313
                                                                                                                                         PRT;
                                                                                                                                                                                                                            Hypothetical protein 1mo0613.
LMO0613.
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Best Local Similarity 29.0%
Matches 102; Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=1639;
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01-MAR-2002
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                                                                                                                                                           Q8Y9B9;
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                                                                                                                                                     At1g23740/F508_27.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SVPTIQKAVIIEG----DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKI---
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Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T.,
Satou I Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                          Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick J. Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.",
Submitted (AUG-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%; Score 261; DB 10; Length 386; 32.2%; Pred. No. 1e-11; tive 37; Mismatches 104; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Arabidopsis ORF clones.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF411799; AAL06488.1; --
EMBL; AY094032; AAM16188.1; --
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Pfam; PF00107; adh zinc; 1.
SEQUENCE 386 AA; 40986 MW; 4DDD19133C9D5D84 CRC64;
                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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386 AA
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                                                                  Created)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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STRAIN-Rwilcz cv. Berken; TISSUE-Hypocotyl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSJNBb0011E04.26 protein.
OSJNBB0011E04.26.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : || : || : || || || || || 110 IAPLPEGIS------QKGEKVLIHAGA 154
                                                                                                                                                                                                                                                                              Character P., Frangeul L., Buchrieser C., Rusnick C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetcuani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant I., Dussurget O.,
Bntian K.-D., Faihl H., Garcia-del Portillo F., Garrido P.,
Cautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maltcurnam A., Mata Vicente J., No E., Nadjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Comparative genomics of Listeria species.";
Comparative genomics of Listeria species.";
EMBL; AL590165; CAC95854.1; -.
Listilist; LIN00622; -.
Listilist; LIN00622; -.
Rabit Prolloy; add zinc; 1.
Ramin Prolloy; add zinc; 1.
Rhypothetical protein; Complete proteome.
SEQUENCE 313 AA; 34007 MW; 659FE9399D7EEEOO CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 VVPDIMGGQIE-TDSYDVLKEG-TGRLVSIVGISNE---DRAKEKNVTAN-GIWLQPNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 KAVIIE---GDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWK----HIAYKIGPE-GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THSTADELSEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGA
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QLKKLGELLANKTVKPIVGAT-FPFSEKGVFDAHALSETHHAVGKIVISFN 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.5%; Score 260; DB 16; Length 3
28.8%; Pred. No. 9e-12;
tive 60; Mismatches 118; Indels
                                                                                             Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Last sequence update)
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                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar 6a;
PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, Auxin-induced protein.
Hypothetical protein lin0622
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Matches 101; Conservative
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SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=1642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 IDSPLPTAPGYDVAGVVVVKVG-NQVKKFQVGDEVYGDINEVTLDHPKTIGSLAEYTAVEE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 PLFYKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHT- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 KV-----LAHKPSN-----LSFVEAASLPLAIITAYQGL------ETAQFSV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 KIGPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKN-GAFAEYARVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 -HPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SVPTTQKAVIIE---GDKAVVKTD--VSVPELKEGTALVKVEAVAGNPTDWK----HIAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GDKAVVKTD--VSVPELKEGTALVKVEAVAGNPTDWKHIAYKI----GPEGSILGCDIAG
Chen J., Wu D., Witham F.H., Heuser C.W., Arteca R.N.; "Molecular cloning and characterization of auxin-regulated genes from mungbean (Vigna radiata) hypocotyls during adventitious root
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota; Viridiplantae; Stroptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzaes; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                         26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 VKIDITLLYRASGOEILLGATRFPASPEYHEATVKFVKFINPHLNNGDI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.9%; Score 248.5; DB 10; Length 309; 32.7%; Pred. No. 6.7e-11; tive 32; Mismatches 102; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC
                                                                                                                                                                                                                                                                                                                                                          Query Match 13.5%; Score 259; DB 10; Length 317; Best Local Similarity 28.9%; Pred. No. 1.1e-11; Matches 101; Conservative 49; Mismatches 143; Indels S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 DLLEKLRPYLENGQ---VKPILDPKSPFPFSQTVEAPSYLKTNRATGKV
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STRAIN=Cv. Nipponbare;
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, clone:OSJNBb0011E04 ";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
SEQUENCE 3493, BAC22575.1; "A5327563A43DB6C5 CRC64;
                                                                                             formation.",
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20808; Q43677; -.
InterPro; IPR002085; Adh_zn_family.
Pfam; PP00107; Adh_zinc; 1.
SEQUENCE 317 AA; 34178 MW; 82C06A0A4AC12793 CRC64;
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Q8ES25;
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                                                                                                              -----LGFAQAGLPLAIETAHEGLERAGFSAGK------SILILGGAGG 161
                                                                                                                                                       VGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHV 241
                                                                                                                                                                                           VGSLAIQLAKHVYGASKVAATASTPKLELLKSLGADVAIDYTKEN-FEDLPDKY---DVV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 DEISEGPVKNFESAASLPVSLTTA--GVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQHVI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSFIIOLAKHVYGASKVAATSSTGKLELIKSLGADVAIDYTKEN-FEDLPDKY---DVVY 218
TVVKLGPNASTDLKVGDTGFGFVHGASQTDPK-NGAFAEYARVYPPLFY---KSNLTHST 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 TVVKLGPNASTDLKVGDTGFGFVHGASQTDPKN-GAFAEYARVYPPL--FYKSNLTHSTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                      15 DKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYKIG-----PEGSILGCDIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 VVLKVGSQVK-DLKEGDEVYGDINDKGLEGPTQFGTLAEYTAVEERLLALKPKNL----
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots;
Asteridae, campanulids, Asterales, Asteraceae, Asteroideae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF384244, AAK66565.1;
IntersPro; IRR002085, Adh zn family.
Pfam; PF00107; adh zinc; 1...
SEQUENCE 309 AA; 33190 MW; EA03340E6CCE6D83 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                         LDAVGQGE---KAVKVVKEGGSVVVLTGAVVP 246
                                                                                                                                                                                                                                 242 IDAVGSEDSIPEAYKVTADSLPATLL -- EVVP 271
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01-MAR-2002
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ol-UCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Quinone oxidoreductase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudioctyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 SEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLI
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SECUENCE FROM N.A.
MEDLINE-22220767 PubMed=12235376;
Takami H., Takati Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from Ridge and its unexpected adaptive capabilities to extreme environments.";
Nucleic Acids Res. 30:3927-3935 (2002).
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY085513; AAM62737.1; ...
InterPro; IPRO0085; Adh.zn.family.
Pfam; PF00107; adh.zinc; 1...
ERQUENCE 309 AA; 32726 MW; 3DAC0046DFE60DAD CRC64;
                                                                                                                                                                                                                                                                                               Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexa
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.,
"Full-length messenger RNA sequences greatly improve g
annotation.";
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Last annotation update)
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Bacteria; Firmicutes; Bacillales; Oceanobacillus.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 IHAGSGGVGSFAIQPAKHFGAY--VATTASGKNESLVKELGADRFINY------K 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 EENFNEVL------EDYDIVVDTLGGDILE-----QSF--EVLKEGGKL----- 232
                                                                                                                                                                                                                                                                                55 GPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLF 114
                                                                                                                                                                                                                                                                                                                                                                                115 YKSNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 IWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 YPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 RASGQEILLGATRFPASPEYHEATVKFVKF------INPHLNNGDIHHMNIK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | : : | | 33 -----VSIAGNPDEEKAKEKGIKAGFLWLEENGKQLSEVADLLENGKVKSVIGH 281
                                                                                                                                                                            8 KAVIIEG---DKAVVKTDVSVPELKEGTALVKVBAVAGNPTDWK-------HIAYKI 54
                                                                                                                                                                                                         MEDLINE 2160850; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monds D.E., Aineida N.F. Jr., Woo L., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Katyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Chunde G., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Bliddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21608551, PubMed-11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houndel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
                                                                                                                               Gape
                                                                                                                            Indels 114;
                                                                            Length 311;
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                          23166D912B5FD248 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Zinc-binding oxidoreductase.
ATU524 OR AGR PAT 466.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                    Query Match 11.4%; Score 219; DB 16; 1
Best Local Similarity 24.9%; Pred. No. 1.2e-08;
Matches 97; Conservative 48; Mismatches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 VFSNGLDDVPALTEGIKEGKNKNVKYVAR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 TF-----PLTEQGLREAHQLSETHHAR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
Complete proteome.
SEQUENCE 311 AA; 34091 MW;
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179 RHSPIPLQGKTVLVNGAGGGVGHLAIQLAKWRGAH--VIAVASGKHBALLRALGADQIID 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 TV------PASELALKPAGIDHIQAAGAPMSLLTAWQPLVDLGHDAPNPFQSF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 WHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AYKIGPEGS---ILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 KAVIIEGDKAVVKTDVSVPEL------KEGTALVKVEAVAGNPTD-----WKHI
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative oxidoreductase (Putative zinc-binding oxidoreductase).
SCO0780 OR 3SCF60.12.
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MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G. Clelo C., Slater S., "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens (588.";
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.4%; Score 218; DB 16; Length 353; Best Local Similarity 29.9%; Pred. No. 1.8e-08; Matches 80; Conservative 36; Mismatches 106; Indels 44
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Streptomycineae, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1916, 1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.coelicolor; STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altenbuchner J.;
"Amplifiable element AUD4 from Streptomyces lividans 66.
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Seeger K.J., Harris D.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 Science 294:2323-2328(2001).

EMBL; AE008954; AAL46012.1; -.

EMBL; AB007901; AAK90698.1; -.

InterPro; IPR002085; Adh_zn_family.

Pfam; PF00107; adh_zinc; 1..

Plasmid; Complete proteome.

SEQUENCE 353 AA; 36922 MW; 618FBE7361FFALAS CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 YHDAGVIEQIKSKYPNLQHVIDAVGSED 249
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MEDLINE=20512582; PubMed=11058132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 K--SNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKWEWHPSTPQHTHPL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 LIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 LVHAAAGGVGHVAVQIAKARGARV-IGTASAAKHE-FLRSLGADETVDYRETDFAEAVK- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 KYPNLQHVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEE-----IRKDNVKI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TQKAV---IIEGDKAVVKTDVSVPELKEGTALVKVEAVAGNPTDWKHIAYK--IGPEGSI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 LGWDVSGVVESVGIGVAA-FRPGDEVFGMLSYPFGH------GSHAEYVTAPARTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                             SPECIES=S.coelicolor; STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch B., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 214; DB 16; Length 313; 26.5%; Pred. No. 3e-08; ive 53; Mismatches 122; Indels 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus. NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                      313 AA; 33213 MW; 44B2871228BB4A84 CRC64;
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Last sequence update)
Last annotation update)
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InterPro: IPR002085; Adh zn family.
InterPro: IPR002184; QOR_zeta_crystal.
Pfam; PF00107; adh zinc; I.
PROSITE; PS01162; QOR_ZETA_CRYSTAL; 1.
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DAD---RAGMEEIARLVGAGRLRAT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86; Conservative
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STRAIN=C-125 / JCM 9153;
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BH0363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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SEOUENCE 313 AA;
                                                                  SEQUENCE FROM N.A
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AC QOSKEV
AC QOSKEV
DT 01-0C
DT 01-0C
DT 01-DC
CON DE QUINO
CON BACIO
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-GCDIAGTVVYLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 GVGTTAIQMAKLLGAGTVIGTVGSADKITAAKESGADEVICYEEEDFTKSV------QE 201
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MEDLINE=21929760; PubMed=11932238;
Galagan J. B., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
Galvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
Allen N., Naylor J., Stangels R., Endring R., Johnson R.,
Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.
Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C.,
Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
Metcalf W.W., Birren B.;
                                                                                                    halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331 (2000).
EMBL; AP001508; BAB04082.1; -.
HISSP; P28304; 1QCN.
InterPro; IPR002085; Adh zn family.
InterPro; IPR002085; Adh zn carystal.
PFam; PF00107; adh zinc; IPR01085.
PFam; PF00107; adh zinc; I.
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                             10.8%; Score 208; DB 16; Length 324; 26.4%; Pred. No. 9.2e-08; ive 53; Mismatches 132; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                            324 AA; 34754 MW; 96690EC3445B79C5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 SCRSVLGPSLGTTR-KCKPHLLKETARHVL---PYLASGKL 290
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Last annotation update)
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les 90; Conservative 5
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
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102 AFAEYARVYPPLFYKSNLTHSTADEISEGPVKN--FESAASLPVSLTTAGVSLCHHLGSK 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 MEWHPSTPQHTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDV 219
                                                                             129 EGPVKNPESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGATAVGQQLIQ 188
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                                                                                                                                                                                                                8 KAVIIEG----DKAVVKTDVSVPELKEGTALVKVEAVAGNPTD-WKHI-AYKIGPE-GSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 343;
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NCBI_TaxID=63363;
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Last annotation update)
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EMBL; AE00735; AAC07327.1; -.

HSSP, 292304; 1QOR.

InterPro; IPR002085; Adh_zn_family.

Pfem; PF00107; adh_zinc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIDVAGVVDAQGP-GEVSFQPGEEVF-----AKVSIGQGSYAEYTVV------ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NSAQVARKPKSIGFVESAAIPTAGLAAWQSLFDIAGL-----EKGQSVLIHGAAG 151
                                                                                                                                                                                                                                                                                                                                                                                      8 KAVIIE--GDKAVVKTDVSVPELKEGTALVKVEAVAG--NPTDWKHIAYKIG--PEGSIL 61
                                                                                                                                                                                                                                                                                                                                                                                                                   2 KAIRIHEFGGKEVWKXE-DIPQPQPGTGEIRIRIAAGVNPWDWKIRSGMIGEMPLPMTM 60
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  genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Non canonical transit peptide for import into the chloroplast."; J. Biol. Chem. 0:00-0(0).
EMBL; AJS11792; CAD5431.1; -. SEQUENCE 329 AA, 34811 MW; 908A03516336890E CRC64;
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Miras S., Salvi D., Ferro M., Grunwald D., Garin J., Joyard J.,
Rolland N.;
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                                                                                                                                                                                                                                                                                     Length 309;
                                                                                                                                                                                                                                                                                10.4%; Score 200; DB 17; Length 30 26.2%; Pred. No. 3.5e-07; ive 52; Mismatches 120; Indels
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29.0%; Pred. No. 4.2e-07;
ive 34; Mismatches 112; Indels
                                                                                                                                                                                                                                309 AA; 33158 MW; D56D002077DA241D CRC64;
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Last sequence update)
Last annotation update)
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                  and physiological diversity.",
Genome Res. 12:532-543(2002).
EMBL; ABC10739; AAM04212.1;
InterPro; IPR002085; Adh zn. family.
InterPro; IPR002364; QOR_zeta_crystal.
PFam; PF00107; adh zinc; 1.
Complete proteome.
SEQUENCE 309 AA; 33158 MW; D56D002077
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QOR.
Spinacia oleracea (Spinach).
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hes 74; Conserv
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122 STADEISEGP-VKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 -PADEVAPKPKAADHIQAGALPLAGLTAWQGLVRHGALK-----SGQRVLVHAAAG 154
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                                                                                                                                                                                                                                                                                                                           GCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPPLFYKSNLTH
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005223; BAC19648.1; -.
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
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                                                                                                                                                                                                     9.8%; Score 189; DB 16; Length 308;
29.0%; Pred. No. 2.4e-06;
Live 28; Mismatches 100; Indels 4.
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NCBI_TaxID=152794;
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                                                                                                                                                           308 AA; 32146 MW; 4E56DFDB90635808 CRC64;
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Last annotation update)
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DNA Res. 7:331-338 (2000).

EMBL; AP003000; BAB49853.1; -
InterPro; IPR002085; Adh zn family.

InterPro; IPR002364; QOR_zefa_crystal.
                                                                                PEGMIP PF00107; adh zinc; 1.
PROSITE; PS01162; QOR_ZETA_CRYSTAL; 1.
Complete proteome.
SEQUENCE 308 AA; 32146 MW; 4ESEDFN
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                                                                                                                                                                                                                             Local Similarity
tes 72; Conserv
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                                                                                                                                                                                                                                                                                            MEDLINE=22295063; PubMed=12397186; Addic D., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y., Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.; "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
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MEDLINB=21083930; PubMed=11214968;
MEDLINB=21083930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 9.9%; Score 190; DB 16; Length 322; Local Similarity 28.9%; Pred. No. 2.2e-06; les 73; Conservative 36; Mismatches 96; Indels 46
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Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                           Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 322 AA; 35607 MW; F73DCA218DEEF906 CRC64;
                                            Last sequence update)
Last annotation update)
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EMBL, AE014908; AANS8375.1; -.
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STRAIN=UA159 / ATCC 700610 / Serotype C;
                       Created)
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208 YPDGFDHIIDTSG 220
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                                                                                           Putative oxidoreductase
                                                                                                                                        Streptococcus mutans
                                                                                                                                                                                  Streptococcus.
NCBI_TaxID=1309;
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                                                                           ---HLVDERLVGHAPGSV-DATHAAALPLVFLTAWEALFDRL------PVTQSTTGTLL 157
                                                175 IWGGATAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSK 234
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MEDINE=97000351; PubMed=8843436;
MEDINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered coosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Crohin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                             235 YPNLQHVIDA--VGSEDSI-----PEAYKVTAD 260
                                                                                                                                                                           213 ISGVDFVFSSWTTGREEELTAVMSPQSHLVLID 245
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EMBL; AL939123; CAB70647.1; -.

HSSP; P28304; 100R.

InterPro; IPR002085; Adh zn_family.

InterPro; IPR002364; QOR_zeta_crystal.

PROSITE; PS01162; GOR_ZETA_CRYSTAL; 1.
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STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed-12000953;
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Best Local Similarity 28.5%
The Conservative
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                                                                                                                                                                                                   53 KIGPEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LFYKSNLTHSTADBISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 LLPP--LPKSV------SYEEGAALAMTPMTAHLSL------PDRGRLQKGET 141
                                                                         LGPNASTDLKVGDTGFG---FVHGASQTDPKNGAFABYARVYPPLFYKSNLTHSTADBIS 128
                                                                                                                                                                       129 EGPUKNFES-----AASLPVSLTTAGVSLCHHLGSKMEWHPSTPQHTHPLLIWGGA 179
                                                                                                                                                                                                                                                                        180 TAVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQ 239
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                                                                                                                    101 TGFGV-TLFRPGDEVFGMLPYPHG-----HGSHABYV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete griome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317,4331(2000).

EMBL, AP001510; BAB04654.1; -
InterPro; IPR002085; Adh_zn_femily.

Pfam; PR00107; adh_zinc; 1.

Complete proteome.

SEQUENCE 312 AA; 34771 MW; B9D16F204BC5CE2E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 322;
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NCBI_TaxID=86665;
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Last annotation update)
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
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Horikoshi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21608550; PubMed=11743193; Mood D. W., Setubal J. C., Kaul R., Monks D. E., Kitajima J. P., Wood D. W., Setubal J. C., Kaul R., Mood G. E., Almeida N. F. Jr., Woo L., Chen Y., Paulsen I. T., Eisen J. A., Karp P. D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M. J., McClelland E., Palmieri A., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon Sampon S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodner B., Hinkle G., Gartung S., Miller N., Blanchard M., Qurcollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sar C., Strub G., Cielo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.7%; Score 187; DB 16; Length 359; 27.5%; Pred. No. 4.4e-06; ive 40; Mismatches 123; Indels 74
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Zinc-binding oxidoreductase.
ATUS447 OR AGR PAT 656
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                         359 AA
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EMBL; AE007913; AAK90822.1; -.
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MEDLINE=21608551; Pubmed=11743194;
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Pfam; PF00107; adh_zinc; 1.
Plasmid; Complete proteome.
                                                                                                                                                  (TrEMBLrel. 21,
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                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                  -JUN-2002
                                                                                                                                                                                                                                                                                                                                                                      Plasmid AT.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 VVRIGQDVK-NFKPGDKVVAMLGSFG------GGGLAEYG-----VASEKLTVH 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 HVIDAVGSEDSIPEAYKVTADSLPATLLEVVPMTIESIPEEIRKDNVKIDITLLYRASGQ 299
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Matvienko M., Torres M.J., Yoder J.I.;
Matvienko M., Torres M.J., Yoder J.I.;
Matvienko M., Torres M.J., Yoder J.I.;
"Transcriptional responses to host root signals by parasitic plants.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF304461; AAG53944.1:
InterPro; IPR02085; Adh_zn_family.
Pfam; PF00107; adh_zinc; 1.
Roon_TER 329 329
                                                                                                                                                                                                                                                                                                                                                            Triphygaria versicolor.

Eukaryochyta; Tracheophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Lamiales; Orobanchaceae; Rhinantheae; Triphysaria.

NCBI_TaxID=64093;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                               288 GVLKKASRRGV--DYSFLFWRAEGQQL 312
SIPEEIRKDNVKIDITLLY-RASGQEI 301
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Quinone-oxidoreductase QR1 (Fragment)
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIKSKYPNLQH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 V--IDAVGSEDSIPEAYK------VTADSLPATLLEVVPMTIESIPEEIRKDNVKI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 GDKAVVKTDVS-VPELKEGTALVKVEAVAGNPTDWK------HIAYKIGPEGSILG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Gaps
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                                                                                                                                                                              Y., Qin Z.,
                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative zinc-binding oxidoreductase.
SCO0419 OR SCF51.18.
Streptomyces coeliolor.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 178.5; DB 16; Length 25.6%; Pred. No. 1.6e-05; tive 48; Mismatches 115; Indels
                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Pu G., Lu L., Lu G., Jia J., Tu Chen Z., Wen Y.;
Submitted (NOY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016744; AA003693.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                           315 AA; 34721 MW; 857F15A32D24DD07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBL_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 AA
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 25.6% Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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62 LTRPKCPVAGLDAAGVVERVGADV-RGFGPGDRVLGFC------PGAFAEYACTTAP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 KAVVK-----KHIAYKIG--- 55
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MEDLINE=2133226; PubMed=11427726;
MEDLINE=2133226; PubMed=11427726;
MEDLINE=2133226; PubMed=11427726;
MAWAYEZ M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Pletcher C., Gordon P.M.K., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KAVVQERPGPPDSLRLRDVDRPHAGAGQVLVRVHAAAVNPYDWHMLRGDPYVARMLGGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PEGSILGCDIAGTVVKLGPNASTDLKVGDTGFGFVHGASQTDPKNGAFAEYARVYPP
SEQUENCE FROM N.A.
STRAINEA3(2) / M145.
STRAINEA3(2) / M145.
STRAINEA3(2) / M145.
Bentley S.D. Chater K.P. Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Cronin A., Praser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Rabbinowitschers D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 MLV------PVPEG--LTFEQAALPMAAVTALRGIRTVGRVRSGQR----
                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417.141-147(2002).
EMBL; A1931916: CABS9116.1;
InterPro; IPR002085; Adh_zn_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%; Score 176; DB 16; Length 329; 28.4%; Pred. No. 2.7e-05; tive 28; Mismatches 78; Indels 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
ON-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alcohol dehydrogenase (Zn containing) (adh-12) (EC 1.1.1.1).
ADH-12 OR SSO2800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64;
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InterPro; IPR002085; Adh.zn.family.
Pfan, PF00107; adh.zinc; 1..
Oxidoreductase; Complete protecome.
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Best Local Similarity 28.4%
Marches 66; Conservative
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completed: January 10, 2004, 10:07:16 ie : 95 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                            137 YT------WEMGSSLTVAALTA----YHALKEAQLSPS-----QTLVVFGASG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AVGQQLIQVAKHINAYTKIVTVASKKHEKLLKSYGADDVFDYHDAGVIEQIK----SKYP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 NLQHVIDAVGSE--DSIPEAYKVTADSLP-ATLLEVVPMTIESIPBEIRKDNVKIDITLL 293
                                                                                                                                                                          21 TDVSVPELKEGTALVKVEAVAGNPTDWKHI-AYKIGPEGSILGCDIAGTVVKLGPNASTD 79
                                                                                                                                                                                                           MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Mond G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Senphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
                                                                                                                 Gaps
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                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2223-2328(2001).
                                                     9.2%; Score 176; DB 17; Length 331; llarity 25.5%; Pred. No. 2.7e-05; Conservative 51; Mismatches 107; Indels 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.
VCTI_TaxID=176299;
331 AA; 36851 MW; A3A1F1F4EE177A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
2inc-binding dehydrogenase.
ATUS188 OR AGR_PAT_262.
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                                                                                                                                                                                                                                                                                         80 LKVGD--TGFGFV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 YRASGQEILLGATR 307
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                                                                                1 Similarity
80; Conserva
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                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 HTHPLLIWGGATAVGQQLIQVAKHINAYTKIVTVASKRHBKLLKSYGADDVFDYHDAGVI 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 PPLFYK--SNLTHSTADEISEGPVKNFESAASLPVSLTTAGVSLCHHLGSKMEWHPSTPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 AAIMRETEGLGUDVVFDTLGGE-----TLSHSPKVLAQF--GRVVSIVDIARPQN-
                                                                                                                                                                                                                                                                                                        93; Gaps
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9.1%; Score 174.5; DB 16; Length 358;
Best Local Similarity 25.2%; Pred. No. 4e-05;
Matches 98; Conservative 50; Mismatches 148; Indels 93;
                                                                            Pfam, PF00107; adh zinc; l. P
Plasmid; Complete proteome.
SEQUENCE 358 AA; 38909 MW; 929D84D9D9ED11C5 CRC64;
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EMBL; AE007889; AAK90558.1; -
InterPro; IPR002085; Adh zn family.
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2 3.9 313096 2 ACI31879 8 3.8 12696 3 PFRAAJ3P3 6 3.8 126906 6 AX655393 6 3.8 125026 10 AC031616 6 3.8 125026 10 AC031616 6 3.8 125026 10 AC0316308 6 3.8 185814 2 AC116417 6 3.8 185814 2 AC116417 6 3.8 185814 2 AC116417 6 3.8 219955 2 AC12414 6 3.8 219955 2 AC12414 6 3.8 219955 2 AC12414 7 3.8 219955 2 AC127414 7 3.8 219955 2 AC127414 7 3.8 219955 2 AC127414 7 3.8 219955 2 AC127414 7 3.8 219955 2 AC127414 7 3.8 249751 3 APPO0399 7 3.8 343751 3 AC136996 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 110000 2 AC11624_2 7 3.8 110000 2 AC11624_2 7 3.8 110000 2 AC13679 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 343590 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.8 34097 1 APO03359 7 3.	Using the reductable between batch (JP)  Daicel Chemical Industries, Ltd. (JP)  Daicel Chemical Industries, Ltd. (JP)  Daicel Chemical Industries, Ltd. (JP)  Daicel Chemical Industries, Ltd. (JP)  Location(Qualifiers  1.1113  / Organism="Kluyveromyces lactis" //mol_type="genomic DNA" //mol_type="genomic DNA" //mol_type="genomic DNA" //mol_type="genomic DNA" //mol_type="genomic DNA" //mol_tare="lacel" //mote="unnamed protein product" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molestare="lacel" //molesta
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Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                            TIGCCAGITICGITGACAACTGCTGGTGTTAGTTTGTCATCATCACTTGGGCTCAAAATG
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 GGTGCATTTGCTGAATATGCCAGGGTTTATCCACCTTTGTTTTACAAGAGTAACTTAACT
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                                                  CACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCTGCATCA
                                                                   CACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCTGCATCA
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Sequence 14 from Patent BP1236796.
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Sy yammanco, H. and Kimoto, K.

Novel enone reductase, process for producing the same, and method for selectively reudcing carbon-carbon double bonds of alpha, beta-unsaturated ketone using the same

DAICEL CHEMICAL INNUSTRIES LTD

OS Kluyvercomyces lactis

PN JP 2002247987-A/1

PD 03-SEP-2002

PP 23-FEB-2001 JP 2001049363

PI HIROAKI YAMAMOTO, KUNIHIRO KIMOTO

PC 012N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/02, C12P7/

PC (C12N15/09, C12R1:645), C12N1/19, C12N1/21, C12N5/10, C12N1-645)

CC NOVEL enone reductase, process for producing the same, and CC
                                                                                             BD174421 lil3 bp DNA linear PAT 18-MAR-2003 Novel enone reductase, process for producing the same, and method for selectively reudcing carbon-carbon double bonds of alpha, beta-unsaturated ketone using the same.
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BD174421.1 GI:29120109
BD174421.1 GI:29120109
SD002247987.4/1.
Kluyveromyces lactis
Kluyveromyces lactis
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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/organism="Kluyveromyces lactis"
/organism="monomic DNA"
ketone using the same Key Location/Qualifiers CDS (1): (1113). Location/Qualifiers
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KIUVYCTOMYCER lactis
Saccharomycetales; Saccharomycetese; KIUVYCTOMYCES;
Saccharomycetales; Saccharomycetese; KIUVYCTOMYCES.
BCATALOMYCEALSES; Saccharomycetese; KIUVYCTOMYCES.
Saccharomycetales; Saccharomycetese; KIUVYCTOMYCES.
Saccharomycetales; Saccharomycetese; KIUVYCTOMYCES.
Saccharomyces for carbon double bonds of alpha, beta-unsaturated ketone using the same beta-unsaturated ketone using the same beta-unsaturated ketone using the same beta-unsaturated ketone using the same beta-unsaturated ketone using the same DAICEL CHRANCAL INDUSTRIES LTD
DAICEL CHRANCAL INDUSTRIES LTD
OA KIUVYCTOMYCES lactis
PN JP 2002247987-A/8
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Pred. No. 1.3e-101;
5; Mismatches 3;
                                                /organism="Kluyveromyces lactis"
/mol_type="genomic DNA"
/db_xref="taxon:28985"
_104 c 108 q 156 t
Patent: EP 1236796-A 14 04-SEP-2002;
Daicel Chemical Industries, Ltd. (JP)
Location/Qualifiers
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23-FEB-2001 JP 2001049363
HIROAKI YAMAMOTO, KUNIHIRO KIMOTO
CIZNIS/09, CIZNI/15, CIZNI/19, CIZNI/21, CIZNS/10, CIZN9/02, CIZP7/
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/organism="Kluyveromyces lactis"
/mol_type="genomic DNA"
/db xref="teaxon:28985"
a 104 c 108 g 156 t
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793 835 853 895

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BD174423 1184 bp DNA 11near PAT 18-MAR-2003 Novel enone reductase, process for producing the same, and method for selectively reudcing carbon-carbon double bonds of alpha, beta unsaturated ketone using the same.
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Saccharomycestles; Saccharomycetes,
Saccharomyces are to 1134)
Sammoto,H. and Kimoto,K.
Novel enone reductase, process for producing the same, and methoc for selectively reuding carbon-carbon double bonds of alpha, beta-unsaturated ketone using the same
L. Patent: JP 2002247987-A 3 03-SEP-2002;
DAICEL CHEMICAL INDUSTRIES LTD
OS Saccharomyces cerevisiae (yeast)
Ph 32-SEP-2002
PP 23-FEP-2001
PP 2002247987-A/3
PP 21-SEP-2001
PP 2002247987-A/3
PP 21-SEP-2001
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JP 2002247987-A/3.
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EYGADELFSTHOIVYGPILLWGGATAVGGSLIQLANKLNGFTKIIVVASRKHEKLLK
RYGENVKKENRRQNVTIDIIRLYSIGGHEVPGNITLPADSEARKAAIKFIKFINPK
INDGQIRHIPPRVXKGNCLOVPHILKDIKYGKNSGEKLVAVLN"
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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3; Mismatches 450; Indels
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/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
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The nucleotide sequence of Saccharomyces cerevisiae chromosome XII Nature, 387 (6632 Suppl), 87-90 (1997)
                                                                                                               974 taaaattratcaaattcatcaatccaaagatraatgatggacaaatrcgccafattccag 1033
                                                                                                                                                                                       1034 TAAGGGTCTATAAGAACGGGCTTTGTGTTCTTCCTCATATCCTAAAAGACATCAAATATG 1093
                                                                                                                                                                                                                                                                                                                                                                      PLN 01-AUG-1997
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Saccharomyces cerevisiae
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
   896 AAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACAG
                                     914 Argadgiaccaritrogaaacarractriraccaeccoacroadaagcraggaaagcrocaa
                                                                             956 TTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCATATGAATA
                                                                                                                                                         1016 TTAAAGTTTTCAGCAACGGCTTAGATGATGTCCCAGCTCTCACTGAAGGTATAAAAGAAG
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Submitted (18-JUL-1997) Saccharomyces Genome Database
5 (bases 1 to 29634)
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URL: http://genome-www.stanford.edu/
e-mail: yeast-curator@genome.stanford.edu
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                                                                                                                                                                                                                                   1076 GTAAAAACAAAATGTTAAGTATGTTGCCAGGTTATA 1112
                                                                                                                                                                                                                                                                       1094 Gradaacrcrggrgaaaaacrcgrrgccgrarraaa 1130
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4 (bases 1 to 29634)
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Kirsten, J.
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Waterston, R.
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This is Neighboring Sequence: This sequence includes nucleotides 1-22200 of cosmid 9122. Washington University

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Retpptehei kethellinriyensdyrpppdlkalreskliktlkaivndpdlgeph
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PTGKGSVLKRPRKYTDRKTERKIRTNRKTPKRRLTKIRTOTIRDVFSNDNENNSKMQNV
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/note="YLR457C; Weak similarity in central portion of the /note="YLR457C; Weak similarity in central portion of the notetien to tropomyosin alpha chain (Swiss Prot. accession number P1642) and kinesin heavy chain (Swiss Prot. accession number P21613)"
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/gene="YLR455W"
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NUMBERKEETQH I PYESHWYMELEDDRKYCH I TRHQKYEHT I LAVDSI A I EERYQLL PDI
LCSANAD I DTLMLDLGSEL PTWYMELSELVHNLDSQLANVEENYFREFYERFASNLQNM
A BCSRNAKCIROKET ILESDEWROQLEDFEDDY IKINIR DI SSTLGARSSYFMERDVFSSV
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FDAXRS SELWGET I I PPHLLDAKFSEVWHLENDYPERSON I FRYSTERFER FFORMSKASTON I FRYSTERFER
FINNSFRANGSYOPALOGTWOCLDNFSKPDLPBSVKLGFWDRYKTELFGKKINIV
WKKGGKFEIS I SKGAKS PYNTHWI I PRODINTSKRYSLEVESSTAGKTI FTDLNF
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DRYTCKP I FPENDNYSHACTLIKWREDARRSAI FFER FYALLSKAYTUK GEREBALKKASSHU
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LFINKENVDLMSNBKLLQRLADTTKANBELKDEDIAKMCDLVYAMEKFVDRIKEK
MYTVDKLQIKOPPLTNHPELLGMNKTISYNLVSNINFNRRRNBERNBCYTLIFBER
DSPFKPSIIMARNIYLNHNRKQLSHTIEPNVSIFYRRRFRNBCTFLIFBER
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LTRRRVLFDYFKCFLPLINMKFTLDDPKFVINDKDDLIIGKFSVFMISHHSKRYTLGN
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EDEELKKYI EKLIIGYDIYDTAQTRKFVNDLHDSEQILAVVEKELLFKRSLLDDIGKL
DLSNIHNERWHQLLRLYILRKVFTSNGNNY INRTLVWNIKVNETILHLLDKIDKPFLD
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                  the rightmost cosmid of chromosome 12. The cosmid on the left is 9324. This sequence overlaps the right telomeric sequence, accession number Z7327, starting at nucleotide 28299.

Location/Qualifiers
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/strain="Sasse( AB972)"
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/note="delta element YLRCdelta27"
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Best Local S:
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/mol_type="genomic DNA"
/db_xref="taxon:4932"
6. 7136
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Pred. No. 2e-69;
0; Mismatches 452;
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                                                                                                1076 GTAAAAACAAAATGTTAAGTATGTTGCCAGGTTATA
                                                                                                                                            15850 GTAAGAACTCTGGTGAAAAACTCGTTGCCGTATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (baker's yeast)
                                                                                                                                                                                                                                                                            DNA
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Daicel Chemical Industries, Ltd. (JP)
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/protein_id="CAD57034.1"
/db_xref="G1:25169910"
                                                                                                                                                                                                                                                                         AX524813
Sequence 3 from Patent BP1236796.
AX524813
AX524813.1 GI:25169909
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Yamamoto, H. and Kimoto, N.
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il Similarity 58.8%;
658; Conservative
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(Ci2N15/09,C12R1:645),C12N15/00,C12N5/00,(C12N15/00,C12R1:645)
Novel enone reductase, process for producing the same, and CC
                                                                Saccharomyces cerevisiae (yeast)
JP 2002247987-A/2
03-SEP-2002
23-FEB-2001 JP 2001049363
HIROAKI YAMAMOTO, KUNIHIRO KIMOTO
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/02, C12P7/
26//
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTA 183
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Location/Qualifiers
1. .1145
/organism="Saccharomyces cerevisiae"
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Pred. No. 2e-69;
0; Mismatches 452;
beta-unsaturated ketone using the same Patent: JP 2002247987-A 2 03-SEP-2002; DAICEL CHEMICAL INDUSTRIES LTD OS Saccharomyces cerevisiae (yeast) PD 2002247987-A/2 PD 03-SEP-2002 PP 201049363 PI HIROAKI YAWAMOTO, KUNIHIRO KIMOTO PC CI2NI5/09, CI2NI/15, CI2NI/19, CI2NI/12 PC C12NI5/09, CI2NI/15, CI2NI/19, CI2NI/12 PC C12NI5/09, CI2NI/19, CI2NI/19, CICNI/10 CC Novel enone reductase, process for p
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/db_xref="taxon:4932"
_245 c 256 g
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(Dasses 1 to 1145)
Yamamoto, H. and Kimoto, K.
Novel enone reductase, process for producing the same, and methor for selectively reudcing carbon-carbon double bonds of alpha,
                                                                                        TTAACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCT
                                                                                                                                                                                                                                                          GTATCCCTCCCAGTCTCATTGACCACGCTGGTATGATCCTTACACATAGTTTTGGCTTG
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Bax-responsive genes for drug target identification in yeast and
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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/db_xref="taxon.4932"
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JANSSEN PHARMACEUTICA N.V. (BE)
Location/Qualifiers
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| O15 ATTABAGTTTTCAGCAACGGCTTAGATGTCCCAGCTCTCACTGAAGGATATAAAAGAA 1074

    (bases 2855 to 2968)
    Michaelis, S. and Herskowitz, I.
    The a-factor pheromone of Saccharomyces cerevisiae is essential for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTTACTTGGTGGACTGTGTCTCCAACACAGAACTATTCAACAGGTGTACAAATGTGCC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   775 GCAGATAGTCTACCTGCCACATTATTAGAAGTGGTTCCAATGACCATTGAAAGCATTCCT 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 895 CAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACA 954
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Bull,P., Thorikay,M., Moenne,A., Wilkens,M., Sanchez,H.,
Valenzuela,P. and Vegas,A.
The yeast tRNA(Phe) gene family: structures and transcriptional
activities reveal member differences not explained by intragenic
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adenosine deaminase; cyclase-associated protein; Fk506-binding protein proline rotamase; mating pheromone alpha-factor 2; mitochondrial outer membrane component; mitochondrial ribosomal protein; NH3 permease; Phe-tRNA; sn-1,2-diacylglycerol cholinephosphortransferase; tyrosine phosphatase.
Saccharomyces cerevisiae (baker's yeast)
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                                                                                  866 GACATGACATGGAAGCCCTCCAAAGCGCAAAGAGAGATCAACCCATCTTATTTTTGGGGTGGT
                                                                                                                                    GCTACAGCAGTGGGTCAACTAATCCAAGTTGCCAAACATATCAATGCTTATACTAAG
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
1 (bases 25310 to 25400)
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                                                                                                     Eukaryota; Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                         European yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCT
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Pred. No. 2e-69;
0; Mismatches 452; Indels
                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-APR-1996) Data collected by MIPS
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/organism="Saccharomyces cerevisiae"
                                                       Saccharomyces cerevisiae (baker's yeast)
                                                                                                                                                                     1 (Dates 1 to 1977)
11 (Dates 1 to 1977)
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/db_xref="taxon:4932"
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LPRFYKKNSNSVSNNNRPSSIFSENLVDFDDVNMVDKTRLFIFLFFFFIIIIPFMV"
                                                                                                                                                                                                                                 Direct Submission
Submitted (29-NOV-1994) Michel Jacquet, Institut de Genetique et
Submitted (29-NOV-1994) Michel Jacquet, Institut de Genetique et
Microbiologie, Universite, Paris-sud, Labotatoire Information
Genetique et developpement, Orsay, 91405, FRANCE
On Jun 14, 1995 this sequence version replaced gi:854489.
Location/Qualifiers
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                   The mitochondrial receptor complex: Mom22 is essential for cell viability and directly interacts with preproteins Mol. Cell. Biol. 15 (1995) In press 12 (bases 7894 to 9190)
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                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Saccharomyces cerevisiae"
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Koser,P.L., Johnson,R.K. and Livi,G.P.
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yeast
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Mol. Cell. Biol. 12 (1), 402-412 (1992)
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Honlinger, A., Kuebrich, M., Moczko, M., Gaertner, F., Mallet, L.,
Bussereau, F., Eckerskorn, C., Lottspeich, F., Dietmeier, K.,
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ATTGTAACTGTTGCTTCTAAAAGCATGAAAAGCTTTTAAAGTCTTATGGTGCTGATGAT
                                                                                                                                                       GTCTTTGACTATCATGATGCAGGCGTTATTGAGCAGATCAAATCGAAGTATCCAAACCTG
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complement(3261. .5483)
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Yeast 9 (7), 753-759 (1993)
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The complete DNA sequence of yeast chromosome III
Nature 357 (6373), 38-46 (1992)
                                                                                                                           Bolle, P.A., Gilliquet, V., Berben, G., Dumont, J. and Hilger, F. The complete sequence of K3B, a 7.9 kb fragment between PGK1 and CRY1 on chromosome III, reveals the presence of seven open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of chromosome III from Saccharomyces cerevisiae reveals seven open reading frames including the RVS161, ADP1 and PGK genes Yeast 8 (5), 409-417 (1992)
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Agostoni Carbone, M.L., Panzeri, L., Muzi Falconi, M., Carcano, C.,
Plevani, P. and Lucchini, G.
Nucleotide sequence of 9.2 kb left of CRY1 on yeast chromosome III
from strain AB972: evidence for a Ty insertion and functional
analysis of open reading frame YCR28
Yeast 8 (9), 805-812 (1992)
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Yeast 8 (8), 681-687 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson, C., Grisanti, P. and Frontali, L.
The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromosome III contains two new open reading frames Yeast B (7), 569-575 (1992)
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   Sor, F.
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The complete sequence of a 9,543 bp segment on the left arm
Chromosome III reveals five open reading frames including
Glucokinase and the protein disulfide isomerase
Yeast 8 (7), 577-585 (1992)
   and
 Benit, P., Chanet, R., Fabre, F., Faye, G., Fukuhara, H. and
Sequence of the sup61-RAD18 region on chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skala, J., Purnelle, B. and Goffeau, A.
                                      Saccharomyces cerevisiae
Yeast 8 (2), 147-153 (1992)
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Yeast 8 (3), 215-222 (1992)
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YCR062w (YCR061w + YCR062w -> YCR061w / C_A563 + C_B120 -> C_B631),
PEP Y, ORF in identical form now C-terminal part of YCR061w,
YCR068w-a (YCR068w + YCR068w + YCR068w -> C_G429 + C_A145 -> C_A520),
YCR068w-a (YCR064w + YCR068w + YCR068w / C_G429 + C_A145 -> C_A520),
YCR0103c (C_F11), former ORF in region corresponding to coord.
307255-307587(C) is obsolete, open reading frame is destroyed by single nt exchange resulting in a stop codon after 45 aa.
NEW GENETIC ENTITIES:
YCL021w-a (C_E193 (YCL027C-a)), PEP Y, new ORF
ALTERED GENETIC ENTITIES:
YCL076w, PEP Y, peptide elongated N-terminally by 51 aa YCL074w,
PEP Y, 3 aa exchanged
YCL076w, PEP Y, 4 aa exchanged
YCL068c (C_F190->C_E560), PEP Y, peptide elongated N-terminally by
70 aa YCL066c, PEP Y, 1 aa exchanged
YCL066c (C_F190->C_E560), PEP Y, peptide elongated N-terminally by
YCL066c (C_F190->C_E560), PEP Y, peptide elongated N-terminally by
YCL066c (C_P190->C_F19096), PEP Y, peptide elongated N-terminally by
YCL061c (C_D853->C_F1096), PEP Y, peptide elongated N-terminally by
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PEP Y, ORF obsolete, is not an ORF in current Chromosome
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Pred. No. 2.5e-67;
0; Mismatches 457; Indels
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58.3%;
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Best Local S:
Matches 651
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304694 CCGATAAACAGGATGCTACCGTTGTCGAATTAACTAATTTGACAGAAAAAGGTCAAAA 304635
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/ DECOLÉTI 16="G1:25169914"

/ LE TABLE 161:25169914"

/ LE TABLE 161:25169914"

/ LE TABLE 16101="MKAVVIDEOKAVVKEGVPI PELEEGFVLIKTLAVAGNPTDWAHI

PENVARSILGCDAAGOIVKLGPAVDPKDFSIGDYI YGFIHGSSYRFPSNGAFAEYS

A1STVVAYKSPNELKFLGEDVLPAGPVRSLEGAATI PV9LTTAGLVLTYNLGLNLKWE

STPORNGPILLWGGATAVGOSLIQLANKLNOFTKI IVVASRKHEKLLKEYGADOLFD

YHDIDVVEQI KHKYNNI SYLVDCVANQNTLQOVYKCAADKQDATVVELTNLTEENVKK

BNRRQNVTIDRTRLYSTGGHEVPFGGITFPADPEARRAATEFVKFINPKISDGOIHHI

PARVYKNGLXDVPRILEDIKLGKNSGEKLVAVLN"
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Saccharomyces cerevisiae
Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Baccharomyces.
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AACATGTTATTGACGCTGTGGGAAGGAAGATAGTATCCCCCGAGGCCTATAAAGTCACAG
                                                                       304754 ceratriasficciacreferecesarcaaatracertreacaacaacrafecac
                                                                                                                                                           CAGATAGTCTACCTGCCACATTATTAGAAGTGGTTCCAATGACCATTGAAAGCATTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            956 TTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCATATGAATA
                                                                                                                                                                                                                                                                                                                          <u> AAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTGTATCGTGCATCTGGTC</u>
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/mol_type="genomic DNA"
/db_rref="taxon:4932"
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Patent: EP 1236796-A 7 04-SEP-2002;
Daicel Chemical Industries, Ltd. (JP)
Location/Qualifiers
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Sequence 7 from Patent EP1236796.
AX524817
AX524817.1 GI:25169913
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Novel enone reductase, process for producing the same, and method for selectively reuding carbon-carbon double bonds of alpha, beta-unsaturated ketone using the same.
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Novel enone reductase, process for producing the same, and CC
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JP 2002247987-A/4
03-SEP-2002
23-SEP-2001
JP 2001049363
HIROAKI YAMAMOTO, KUNHHIRO KIMOTO
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/02, C12P7/
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Saccharomyces cerevisiae
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomyces
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomyces
Saccharomyces Cerevisiae
Saccharomyces Saccharomyces

1 (bases 1 to 1122)
Tamamoto,H. and Kimoto,K.
Novel enone reductase, process for producing the same, and for selectively reudcing carbon-carbon double bonds of alph beta-unsaturated ketone using the same
Fatent: JP 200247987-A 4 03-SEP-2002;
DAICEL CHEMICAL INDUSTRIES LID
S Saccharomyces cerevisiae (yeast)
F 2002247987-A 4
FD 03-SEP-2002
FP 22-FEB-2010 JP 2001049363
FI HIROAKI YAMAMOTO, KUNIHIRO KIMOTO
FC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/07
FC (C12N15/09, C12R1:645), C12N15/00, C12N15/00, C1
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/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"
a 239 c 255 g 298 t
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Location/Qualifiers
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DEFINITION
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ORIGIN
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VERSION
KEYWORDS
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AUTHORS
TITLE
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Direct Submission

Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (8-mail:
2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (8-mail:
3 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (8-mail:
4 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces Riuyverzii, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta. Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers

1. 1083
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/note="similar to Saccharomyces cerevisiae ORF YLR460c
similarity to C.carbonum toxD protein ]
similar to Saccharomyces cerevisiae ORF YNL134c [
similarity to C.carbonum toxD gene ]"
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                       Wincker, P. and Weissenbach, J. Genomic exploration of the hemisscomycetous yeasts: 1. A set of genomic exploration of the hemisscomycetous yeast species for molecular evolution studies

FBS Lett. 487 (1), 3-12 (2000)
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  Tekaia, P., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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de Montigny, J., Straub, M., Potier, S., Tekaia, F., Dujon
Wincker, P., Attiguenave, F. and Souciet, J.
Genomic exploration of the hemiascomycetous yeasts: 8.
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/mol_type="genomic DNA"
/strain="CBS 732"
/db_xref="taxon:4956"
/clone="ARQAAQ29E02"
/clone lib="ARQAA"
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GATGTTCTACCTGCGGGCCCTGTCAGGTCTTTGGAAGGGGCCACCTATCCCAGTGTCA 429
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                                                                                                                                                                                                      CTGACCACAGCTGGCTTTGACCTATAACTTGGGCTTGAACCTGAAGTGGGAGCCA 489
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Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
1 (Dases 1 to 1083)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotchin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Brottier, P., Caparegola, S.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
                                                                                                                                                                                                                                                                               GCAGGCGTTATTGAGCAGATCAAATCGAAGTATCCAAACCTGCAACATGTTATTGACGCT
                                                                  GATGAAATTICTGAAGGCCCTGTGAAGAACTICGAATCTGCTGCATCATTGCCAGTTTCG
                                                                                                                                                         TTGACAACTGCTGGTGTTAGTTTGTGTCATCACTTGGGCTCAAAAATGGAATGGCACCCA
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Genoscope.

Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exigus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyverzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of Location/Qualifiers
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
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/note="similar to Saccharomyces cerevisiae ORF YNL134c
                                                                                 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000) 20584711
                                                                                                                                                                                                                                                                Casaregola, S., Lepingle, A., Bon, E., Neuveglise, C., Nguyen, H. Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts: 7. Saccharomyces servazii: PEBS Lett. 487 (1), 47-51 (2000)
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/strain="CBS 4311"
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                                                                                                                                                                                                                                                                                                      373 TCAGATTCCCGTGTTTTGAGCGGTAAACAGGAGTTACCTTCAGGACCAGTTTCTAATATA 432
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                                                                                                                                                                                                                                          CACTCAACTGCTG-------ATGAAATTTCTGAAGGCCCTGTGAAGAACTTC
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                                                                                    13 others
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similarity to C.carbonum toxD gene
1 putative frameshift(s)"
                                                                                                                                                                      Query Match 9.3%; Score 103.6; DB 11; Best Local Similarity 49.5%; Pred. No. 1.1e-12; Matches 303; Conservative 4; Mismatches 301;
                                                       /evidence=not_experimental
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942 bp DNA linear STS 10-JAN-2001
TT end of clone ATOAA001G11 of library ATOAA from strain CBS 4311
Of Saccharomyces servazzii, sequence tagged site.
AL402417
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Eukarycta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 942)
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Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
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QPFYAFILCIGWIVLTKPYPSLGDAGFFFSFLPPFFTPLFGYLRYPIISALLFLHAIVL
APIFYHLWVVLGSGNSNFFYAISLVYALAIASILVDLNWAMLRIEYDNGIPNFFLKYT
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/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"
2540. .3724
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Bi,E. and Pringle, J.R.
Sequencing and characterization of CDC91
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| proteIn | id="AAA34487.1"
| db_xref="G1:469466"
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                 725 TTGACGCTGTGGGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACAGCAGATAGTC
  Gapa
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JANSSEN PHARMACEUTICA N.V. (BE)
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:5476"
174 c 223 g 330 t
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Sequence 557 from Patent WO02064766.
AX536956.1 GI:25263391
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3 (bases 1 to 1506)
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                                                                                                                                                                                                                                                                                                                                                                             544
TGGGTTCTCAAG---TAACTGGGTTTGCAAAAGGTGACACTGTAAGTGCTTTTAATTG 265
                                    GTGCTTCCCAAACAGATCCTAAAAATGGTGCATTTGCTGAATATGCCAGGGTTTATCCAC 334
                                                                         GTA-----ATAGATCACCTCGCACTGGAGCTTTTGCAGAATATGTAGCTGTTGATCCTG 319
                                                                                                              CTTTGTTTTACAAGAGTAACTTAACTCACTCCAGTGATGAAATTTCTGAAGGCCCTG 394
                                                                                                                                                   CTACTICGATAAAGTACAATAAGAATTTTGAACATTTGACTAATTTACAAGTATCTGAAA 379
                                                                                                                                                                                                                          380 TCCACTCATTTGAAGGGGCAGCAAGTATTAATTTAGGTTTGGTTACCGTTGGGCTTTCAT 439
                                                                                                                                                                                                                                                                                                    440 TTTCTCATTACTTACGAATTGACAAAAAAGCAACC--------TGGGGATA 484
                                                                                                                                                                                                                                                                                                                                                                                                              575 ATATCAATGCTTATACTAAGATTGTAACTGTTGCTTCTAAAAAGCATGAAAAGCTTTTAA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                       601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAATTAGGGGCAGATTATGTTTTCGATTATGGAGACGCTGATGTTGTCAATAAATTA 661
                                                                                                                                                                                                                                                                                                                                                                            GTATITITGATITIGGGGAGGAGCAACTGGAGTTCTAGCCATTCAGGTTGCCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTCTTATGGTGCTGATGTCTTTGACTATCATGATGCAGGCGTTATTGAGCAGATCA
                                                                                                                                                                                       TGAAGAACTICGAAICTGCTGCATCATTGCCAGTTTCGTTGACAACTGCTGGTGTTAGTT
                                                                                                                                                                                                                                                                                                                                         515 CATTATTGATTTGGGGTGGTGCTACAGCAGTGGGTCAACAACTAATCCAAGTTGCCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   545 TAGTGTA---TAATCTCAAAGTAATCACCACAGCATCACCCAAAAACCACACCCTCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi, Ascomycota, Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; Cochliobolus.

1 (bases 1 to 1506)

Tokng, Y.Q., Ahn,J.H. and Walton,J.D.

Toxb, a gene cloned from a HC-toxin producing strain of Cochliobolus carbonum, has no role in HC-toxin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Cochliobolus carbonum"
/mol_type="genomic DNA"
/db_xref="taxon:5017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'chromosome="largest (3.5 Mb)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1506 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="toxD"
289. .110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxD gene.
Cochliobolus carbonum
Cochliobolus carbonum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .carbonum toxD gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:1027510
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
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1 (Dases 1 to 212955)

Nuzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Blankenburg, K., Blyth, P., Brown, M.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y., Chen, Y.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Dapan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K.,
Fagen, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Gancia, R., Garcia, M., Guevara, W.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
                                                                                                                                                                                                                            /translation="MTFQKAIVTEAPHRARLVSDRLIPKLRDDYILVRTVSVALNPTD WKHILRLSPPGCLVGCDYAGIVEBVGRSVKKPFKKGDRVCGFAHGGNAVFSDDGTFAB WITVKGDIQAMIPENLSFPGBATLGWGIKTVGGGLYQSLKLSWPTFBHAVPILIYG GSTATGTLAIQLAKLSGYRVITTCSPHHFELMKSLGADLVFDYHBITSADHIRRCTQN KLKLVFPTSIDVSTROTSBVSRRCDRANSTEGGBYSALLDVSIARTNISSRWTLAYTUGBGFFFSEQIVEQPXPTTMSSGRNFGM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 TIGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                        note="unique to isolates that make the cyclic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 TTCCCAAGTTGAGAGACGATTACATACTCGTCAGGACGGTAAGTGTTGCTCTTAACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 CTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 CTGATTGGAAGCATATTTTGCGT---CTCTCACCCCCAGGCTGTCTGGTTGGCTGCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 ACGCTGGCATCGTTGAGGAAGTAGGCAGGAGTGTTAAAAAACCGTTCAAAAAAGGTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 CCGGTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCATTTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 GAĞTAİĞEĞEÇITTĞETEREĞGGGGTAATGEAĞTTTTTEĞAĞATGATĞGAAÇATTYGEÇE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 TTCCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53.2; DB 8;
Pred. No. 0.19;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus clone CH230-141C19, ***, 2 unordered pieces.
                                                                                              /codon_start=1
/protein_id="CAA63129.1"
/db_xref="GI:1027511"
/db_xref="SWISS-PROT:P54006"
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HTG; HTGS_PHASE1; HTGS_DRAFT;
Rattus norvegicus (Norway rat)
function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 4.8%; al Similarity 54.1%; 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 c
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                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "vorking draft" sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AAGGAGGCTACAGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAG 144
                     Estimated insert size: 210228; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156322 GCTGCTGTTATTGCAGTTGCTGCTGCTGCTGCTGTTCCTGTTGTTGCTGCTGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 TTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCATTTGCTGAATATGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 CATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 GITGICAAACTIGGACCAAAIGCIAGIACTIGACTIGAAGGITGGAGAIACCGGITTCGGI
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4.4%; Score 48.6; DB 2; Length 212955;
Best Local Similarity 47.5%; Pred. No. 1.5;
Matches 144; Conservative 0; Mismatches 159; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 158013: contig of 158013 bp in length
158014 158113: gap of unknown length
158114 212955: contig of 54842 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6243 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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clone_end:T7"
159306. .1613.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end sequence:RWAXI22TJB"
39881. .41507
/note="wgs_end_extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wgs_end_extension
clone_end:T7"
158114. .159255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end_sequence:RWAXI22TJC"
3361. .4184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA'
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3356, .4203
/note="clone_boundary
clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336I. 4184
/note="clone boundary
clone end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="CH230-141C19"
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ORIGIN
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The sequence in this sequence version replaced gi:25188698.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs stated beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvay, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harnandez, J., Harnandez, J., Harnandez, J., Hollins, B., Homelis, S., Hiddun, S.L., Hodgson, A., Hoguses, M., Hollins, B., Homelis, S., Hiddun, S.L., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jackson, L., Jackson, L., Jackson, E., Hume, J., Lewis, L., Loulse, M., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kally, S., Khan, J., Lewan, J., Lewis, L., Liu, Y., Loulseged, H., Lordance, R.J., Lux, M., Man, J., Martin, M., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Pologer, R., Polodecter, R., Polodecter, R., Polodecter, R., Reeves, K., Regier, M.A., Reigh, R., Sanders, W., Savety, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Sheetty, J., Shvatebeyry, A., Siason, I., Street, C.D., Smajs, D., Sheetty, J., Shvatebeyry, R., Trejos, Z., Usmani, K., Tahag, A., Street, M., Street, R., Willes, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Walse, R., Marten, R., Marten, R., Marten, R., Walse, R., Walse, R., Marten, R., Marten, R., Walse, R., Marten, R., Walse, R., Marten, R., Walse, R., Marten, R., Walse, R., Marten, R., Walse, R., Marten, R., Walse, R., Marten, R., Marten, R., Marten, R., Marten, R., Marten, R., Santh, H., Wa
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Submitted (07-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

A (bases 1 to 212955)

Rat Genome Sequencing Consortium.
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Web site: http://www.hgsc.bcm.tmc.edu/
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Rat Genome Sequencing Consortium.
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AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS TITLE JOURNAL

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TESTAKLGITCURSDANRUPATATAAATATATTGEISSRVAALAGLGHHYARCYWELS
KAKLSMLVNATSGTCYILGTGNAAISFPGICYTGGTWGTASANSIMQIPEISNDSK
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LAAATAFSFYRDRTWHKARKWFHABILFLPVFWSGILLHRVSNDNQQQLVEBAGLTN
2606. .4019
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db_xref="GI:20191028"
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                                                                                                                                                                                                                                                             AC003672 109375 bp DNA linear PLN 11-MAR-2002
Arabidopsis thaliana chromosome 2 clone F16B22 map m336, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .709,859. .996,1097. .1230,1352. .1477
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 109375)
Rounsley, S.D., Kaul, S., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA 3 (bases 1 to 109375) Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: F16822.1; supported by cDNA:
gi 15028298 gb AY045952 1 "
join(105. 4895,577. 709,859. .996,1097. .1230,1352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-FEB-2002) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598391.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .13432
/note="overlap with BAC clone F411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 109375
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="F16B22"
                                                                                                                                                                                                                                                                                                                                                    AC003672.3 GI:20197021
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                                                                                            759 GG 760
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287 GK 286
                                                                                                                                                                                                                                                                                                                sequence
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KEYWORDS
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TITLE
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AUTHORS
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AC003672
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                                                                                                                       PAT 22-MAR-2003
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Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
Plant genes involved in defense against pathogens
Patent: WO 0300898-A 5263 03-JAN-2003;
Syngenta Participations AG (CH)
Location/Qualifiers
                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 YSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKGST 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 947 GRWRWRMAWCWYCCMWKWWKWTSCMWWKYWRTWSCWYTMWWGAMRYAYYAMRRRRWTYKW 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 TGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAACAGATCCTAAAAATGGTGCATTTGCTGAATATGCCAGGGTTTATCCACCTTTGTT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CTTCGAATCTGCTGCATTTGCCAGTTTCGTTGACAACTGCTGGTGTTAGTTTGTGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581 ATGCTTATACTAAGATTGTAACTGTTGCTTCTAAAAAGCATGAAAAGCTTTTAAAGTC-- 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 AAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGGTGCTTC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          587 RRSKMGRWSGMSRMYMRWWKKOMRKRKRKYMRYMKWKCTWRRCMCYRWGYTMYTTSRSRMMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #67 MMMYWYRKYSKWMRMSTKYMWSMWYKKCRSMKYGAKGCYGCKMWTYCSYGYMKWYTYMGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 GGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 ATCACTTGGGCTCAAAAATGGAATGGCACCCATCTACCCCGCAACATACTCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 TGATTTGGGGTGGTGCTACAGCAGTGGGTCAACAACTAATCCAAGTTGCCAAACATATCA
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8.6%; Pred. No. 2.2;
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                                                                                                                       linear
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                                                                                                                         DNA
                                                                                                                       AX655393 2000 bp DN.
Sequence 5263 from Patent WO03000898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa"
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/db_xref="taxon:4530"
265 c 284 g 365
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                                                                                                                                                                   AX655393
AX655393.1 GI:29158207
    156022 GTT 156020
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Best Local Similarity
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                                                                                                                                        DEFINITION
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AX655393/c
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AUTHORS
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/gene="At2g44570"
/gene="At2g44570"
/notes="Bynonym: P16B22.6"
complement (join (<14935. .15252,15445. .15729,15807. .16460,
1657. .>16779)
/gene="At2g44570"
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                                                                                                                                                                                     AWDDKFVGAQVLVAKKALEGKVESSEGIVEYKSMAEGFICNCAQKGDNNVKKFPGGLL
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COMPLEMENT (12444. . 14164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEAQRSGKLPSNORVTWRGDSALRDGSDAHVDLTGGYYDAGDNWKFGFPLAFFTTMLA
WSNIEMATQLKAHQEQENALAALKWATDFLIKAHPEPNVLYGQVGDGNSDHECWMRPE
DWTTPRPSFRIDAQHPGSDLAGETAAAMAAASIAFAPSDEAYAQILIGHAKELPEFAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYPGIYQNSITNAGGEYASSGYEDELLWAAAWLHRATNDQIYLDYLTQASGTGGPRTA
FSWDDKFVGAQVLVAKLALEGKYESNGKIAEYKAMEQFICNCAQKGSNNVKKTPGGL
YFTPWNNLQYTTAATFVLASYSKYLTDAKASIQCPNGALQASDLLDLARSQVDYILG
SNPQNMSYWYGVGTRYPKKEHIRAASIVSITKOKTPVTCSEGPDAWFNNPAPNPULM
GAVVGGPNDNDVYGDERTDYQHAEPAPATAAPFVGVLAAVA"
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13943. .>14164))
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13943. .14164))
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16557. .16778)}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(TA)n"
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Best Local Similarity
Matches 116; Conserv
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RLSSGLFGBVIITHTPLSERMYFPQLTVLSVARLHGGSRREYYACTTHAVFSPPAIS
complement (6742. 6763)
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DMTTPRTSYRIDAQHPGSDLAGETAAAMAAASIAFAPFDKAYANILIGHAKDLFAFAK
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FAWDDKFVGAQVLMAKLALERKVGSNGKIAEYKSMAEQFICNCAQKGSNNVKKTPGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSQSKNGSSQCLWTSICIVVLVMSMARGAVSTNYAEALQKSLLY
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3744. .4019)
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/note="synonym: P16B22.3"
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/gene="At2g44540"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALVGGPNENDVYGDERSNFQQAEPATVTVAPFVGVLAAVF"
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                                                                                                                                                                                                                                                                                                                                                                                                    Childress, D., Zeng, Q. and Smith, D.R.
Childress, D., Zeng, Q. and Smith, D.R.
Direct Submission
Submitted (24-JUL-2001) GTC Sequencing Center Production,
Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Waltham, MA 02453-8443, USA
Location/Qualifiers
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/db.xref="G1:15023319"

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YKKNQLLKFEEEINDLQCPVLNRIINEKNT"
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LLSASTNVILRITGMMMKLEEKVSIEEIKSIVEAGQEYGVINESEKEMIDSIFEFDD
RIAEEVMTPRTEVYLINIDTPLNKYVDELLEIKYSRVPVFEGDSDNIIGILYIKDFIV
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                                                                                                                            1 (bases 1 to 13844)
Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q.,
Solbson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I.,
Tatuson,R.L., Sabathe,F.,
Daly,M.J., Bennett,G.N., Koonin,E.V. and Smith,D.R.
Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum
J. Bacteriol. 183 (16), 4823-4838 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="CBS-domain containing protein, YHDP B.subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="Mercuric resistance operon regulatory protein,
                                             Clostridium acetobutylicum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="Protein of short-chain alcohol dehydrogenase
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                   Clostridium acetobutylicum
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                                               ORGANISM
                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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KEYWORDS
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PFMALIPZ_2 200001 384550
PFMALIPZ_3 300001 384550
CONTINUATION 74 Of 9) Of PFMALIPZ from base 300001 (AL031745 Plasmodium falciparum DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19788 AAAATTAAATTAGTTTATTTAATTTGTAAAGCTCGTTTACAATTAATAGTTGGTACAACAA 19847
                                                                                                                                                                                    19848 TCTCTCCCTATGAACAATAATAAAACAAATACAAATAAAACATCAAAAAAATGAATAGTC 19907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32339 GTCATAATATTTTGAGGAGAAAAGAAATCTAAAAGATCTTTTGAAAATAATAATT 32398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32459 TAGATAATGTTTTATCTAATĆTGTAGTGATAACAATATGTGTGGTGATGATATATATAT 32518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE007561 13844 bp DNA linear BCT 27-JUL-2001 Clostridium acetobutylicum ATCC824 section 49 of 356 of the Complete genome. AE007561 AE001437 AE007561.1 GI:15023317
                         AAATTGATATTACTTTGTTGTATCGTGCATCTGGTCAAGAAATTCTATTGGGTGCAACAA 919
                                                                                                                                 920 GATTTCCTGCTAGTCCAGAATATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 AAGTIGCCAAACATATCAATGCTTATACTAAGATTGTAACTGTTGCTTCTAAAAAGCATG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    623 AAAAGCTTTTAAAGTCTTTATGGTGCTGATGATGTCTTTGACTATCATGCAGGCGTTA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            683 TTGAGCAGATCAAATCGAAGTATCCAAACCTGCAACATGTTATTGACGCTGTGGGAAGCG 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    743 AAGATAGTATCCCCGAGGCCTATAAAGTCACAGGATAGTCTACCTGCCACATTATTAG 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                923 TICCIGCIAGICCAGAAIAICAIGAAGCCACAGITAAAATICGITAAAGTITATAAATCCAC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32279 GTGATGATAATAATAATAATAATTGTCATGATAATAATAATGATGATGATCTCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAAAAA
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                                                                                                                                                                                                                                                                                               19908 ATTACTITICCAGAAGITITIACTGCAGTTAACAATAACGTAGTCCAG 19956
                                                                                                                                                                                                                                         980 CACACCTTAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAG 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS PFMAL1P2 Accession AL031745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 84550;
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0; Mismatches 299; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47.6;
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210000
310000
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Begin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 43.3%;
Matches 227; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence split into 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragment Name
                      860
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WPCOMMENT
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    ISVAALTVGALAPIYAFKIVPNLRATCVTLSSVVNGIAQILMTIFIDPQMSIMTEEVM
EKKCSEEDFKNCVLAMVGSKVAGTFAAIFILIPASFAIVFVAKGVDFISRI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   869 ITACTITGTTGTATCGTGCATCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCAATGACCATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producE="Spore maturation protein A (gene spmA)"
protein id="AAK78449.1"
db_xref="GI:15023327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="Spore maturation protein B (gene spmB)"
protein_id="AAK78450.1"
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                                                                                                7119. .7823
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                                                                                                                                                                                                                                                                                                                                                                RRIKSIRNLKQLEBIV"
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                                                      .7823
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Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                   SVESPITKASKKVLPSVVGVTTYIERDNTKKEGVGSGMIIDSSGYILTNNHVAGMTS
KDLKVGLYDGSSIGAKPLMANESLDLSIIKIDKNNLQAVTGDSSKVDIGETAIAIGN
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GIYVYNISPNSGAAAAGINKGDIILSVNGKNINTMNELRESIYTIGANNTVSLKKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /crānelation="MKDSNLEIKILKNKIYDETSSIFIHNLKKLIQLEGTQKKLASKI
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SKGVMFFSLEKSIPRLVYHSMTRRGIYSMKQCVVLPSRKSVEKFNYRKLPRRIIVYNF
                                                                                                                                                                                                                                     product="Serine protease Do (heat-shock protein)"
protein id="AAK78443.1"
db_xref="GI:15023321"
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| Mb xref="01:15021312"
| translation="MOINOPKX EIFIPKEYVEKLGDKLSEANVGKIGNYDHCMATNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="Protein, related to divalent cations, tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
product="Uncharacterized membrane protein, homolog of
YDAH B.subbliis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transT_table=11
/product="Predicted transcriptional regulator,
dicA/hipB/ansk family"
/db_xref="G1:15023323"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAK78447.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4841. .5632)
/gene="CAC0465"
                                                                                                complement (3180. .4226)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4351. .4692
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4351. .4692
/gene="CAC0464"
/codon start=1
/transT_table=11
                                                                                                                                                                                           codon start=1
transl_table=11
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                                                                                                                                                                       gene="CAC0463"
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/gene="CAC0467"
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/gene="CAC0466"
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gene="CAC0466"
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/gene="CAC0467"
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On May 11, 1999 this sequence version replaced gi:4678553.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projectsf/ elegans/wormpep This sequence is the entire insert of clone RP5-106901 The true left end of clone RP4-738116 is at 92256 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mis subclone; and the assembly was confirmed by restriction digest. This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.snager.ac.uk/HGP/Chr20

RP5-106901 is from the library RPC1-5 constructed by the group of Pieter de Jong. Por further details see http://www.snager.ac.uk/HGP/Chr20
HSJ106901 92357 bp DNA linear PRI 04-APR-2001 Human DNA sequence from clone RPS-106901 on chromosome 20. Contains part of the gene for a novel protein similar to a low density AL049633
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 92357)
                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-WAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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note="LIMC5 repeat: matches 7312. .7409 of consensus"
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/note="LINGS repeat: matches 7560. .7913 of consensus"
6803. .680.
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note="L2 repeat: matches 2480, .2735 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2708 of consensus"
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/db_xref="RZPD:RPCIP7040011069"
/db_xref="taxon:9606"
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note="L2 repeat: matches 2653.
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/note="match: STS: Em:L16330"
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/clone_lib="RPCI-5"
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                                                                                                                                                                                 HTG; LRP16.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                    Homo sapiens
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note="MER69 repeat: matches 2426. .2505 of consensus"
.9985. .20378
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/note="MER34 repeat: matches 64. .168 of consensus" 26540. .28647
                                                                                                                                                                                                                                                                                     /note="12 repeat: matches 2642. .2749 of consensus"
10724. .10795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MER5A repeat: matches 11, .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2125. .2253 of consensus"
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6557. .16805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L2 repeat: matches 2689. .2748 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2697 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2384 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MER5B repeat: matches 44. .147 of consensus"
                           853. .7163
note="AluSq repeat: matches 1. .312 of consensus"
                                                                                                                                                                              )307. .9684
'note="THELC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 181. .252 of consensus"
complement (11896. .12355)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7067. .17516
note="MLT2B repeat: matches 1. .444 of consensus"
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'note="MER5B repeat: matches 7. .49 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                 .130 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .123 of consensus"
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                                                                                                                                                                                                                                                    .90 of consensus"
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                                                                                                                                                                                                                                                                                                                                                             omplement (11896. .12355)
note="match: STS: Em:HSPF12C11 Em:294565"
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                                                                                                             7705. .9306
/note="THE1C-internal repeat: matches 1.
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copies 2 mer tt 75% conserved"
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                                                                                          .371
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note="MIR repeat: matches 175.
8990. .19101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L2 repeat: matches 2598.
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5568. .25664
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                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 36.
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2904. .13054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluY repeat: matches 1.
                                                                                                                                                                                                                      9687. .9770
/note="5S repeat: matches 7.
                                                                                      'note="THEIC repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20395. .20462
'note="MER69 re
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12769 CTÁTGTAÁÁAAAGTTACAÁTTTAAÁAATGÁÁTAÁTAACTTÁTTÁTATÁTCÁAGGAAAÁGÁA 12828
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-JUL-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA on Oct 11, 2000 this sequence version replaced gi:9954568.

* NOTE: This is a "vorking draft' sequence. It currently consists of a contige. The true order of the pieces is not known and their order in this sequence record is
                                                                              ACUUBUS7 119082 bp DNA linear HTG 11-OCT-2000
Homo saplens chromosome 20 clone P1-10263, WORKING DRAFT SEQUENCE,
3 unordered pleces.
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                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119082)
McCombie,W.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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22465 c 21882 g 36187 t
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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  6538 AATATATACGG 6550
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Matches 102, Conservative
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                                                                                                                    note="Tigger3b repeat: matches 7. .1228 of consensus" 3105. .33174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Alusx repeat: matches 1. .295 of consensus" 3341. .43987 note="LIMB6 repeat: matches 5488. .6171 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LIMC4 repeat: matches 7218. .7522 of consensus"
/note="L1MA3 repeat: matches 4167. .6304 of consensus"
                                          .6300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACAGCAGATAGTCTACCTGCCACA
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note="MER63 repeat: matches 988. .1050 of consensus"
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note="MER47A repeat: matches 29. .364 of consensus"
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note="MER63 repeat: matches 641. .988 of consensus"
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                                                                              'note="LTR37B repeat: matches 1. .468 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                     7957. .38255
note="MLTII repeat: matches 72. .410 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2707 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 1377. .1805 of consensus"
2557. .42851
                                                                                                                                                              .2737 of consensus"
                                                                                                                                                                        3500. .35623
/note="12 copies 2 mer as 100% conserved"
35695. .35860
/note="WIR repeat: matches 23. .186 of consensus"
35966. .36119
                                                                                                                                                                                                                                                                                                                                           7805. .37859
note="MIR repeat: matches 49. .115 of consensus"
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note="Aluy repeat: matches 1. .304 of consensus"
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Pred. No. 2.9;
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                29755. .30565
/note="LIMA4 repeat: matches 5473.
                                                                                                                                                                                                                                                                                                                      note="MER58A repeat: matches 81. 7805. .37859
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8261. ,48573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="LTR16C repeat: matches 86.
                                                                                                                                       13105. .33174
/note="L2 repeat: matches 2671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L2 repeat: matches 2362. 1385. .41697
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AE014817.1 GI:23
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L Submitted (12-May-1999) Lite Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA

E (Dases I to 169494)

S de la Bastide, M., Gnoj, L., Dedhia, N.N., Matero, A., Ning Huang, E., O'Shaugnessy, A., Preston, R., Rodriguez, M., Schutz, K., Shah, R., Shekher, M., Spiegel, L., Swaby, I., Vill, D. and McCombie, W.R.

Direct Submission

L Submitted (02-JUL-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NX 11724, USA

S MCCombie, W. Richard.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thio Transposon removed.

On Nov 21, 2000 this sequence version replaced gi:5332384.

Clone Pi-7739 contains a 3 kb overlap with Clone 48F5. The overlap ends at base 2940. From position 154930-155350 the subclones were single stranded and had single chemistry.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     736 GGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACAGCAGATAGTCTACCTGCCACA 795
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                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 169494)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Transposon, totalling 1328bp, was removed from final
Homo sapiens chromosome 20 clone Pl-7739, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 47.4; DB 9; Length 169494; 52.8%; Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (18-NOV-2000) Cold Spring Harbor Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-NOV-2000) Cold Spring Harbor Laboratory
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31812 c 32399 g 52939 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="P1-7739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In10 Transposon removed.
1 (bases 1 to 169494)
4CCombie, W.Richard.
                                             AC007630.4 GI:11245571
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                                                                                   Homo sapiens (human)
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102; Conservative
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                                                                                                                                                                            Accombie, W. R.
                                                                                                       Homo sapiens
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Matches 10
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RESULT

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Eukaryottan Alvodata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 254449)
Gardner,M.J. Hall,N., Fung,E., White,O., Berriman,M., Hyman,R.W.,
Gardner,M.J., Hall,N., Fung,E., White,O., Berriman,M., Hyman,R.W.,
James,K., Eisen,J.A., Rutherford,K., Salzberg,S.L., Craig,A.,
Kyes,S., Chan,M.S., Nene,V., Shallom,S.J., Suh,B., Peterson,J.,
Mather,M.W., Vaidya,A.B., Martin,D.M.A., Fairlamb,A.H.,
Fraunholz,M.J., Roos,D.S., Ralph,S.A., McFadden,G.I.,
Cummings,L.M., Subramania,G.M., Mungall,C., Venter,J.C.,
Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and
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DINSFGYSIDAACGQLYADYEPKRKEKIESKNMSLLL"
114. .15150
7.rpt_type=tandem
2423. .2460
7.rpt_type=tandem
7.rpt_type=tandem
7.rpt_type=tandem
7.rpt_type=tandem
2918. .2947
7.rpt_type=tandem
2945. .2973
AE014817 254449 bp DNA linear INV 07-OCT-2002 Plasmodium falciparum 3D7 chromosome 14 section 2 of 13 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein_id="AAN36678.1"
'db_xref="GI:23497130"
'translation="MEKSKRYISLIKMMERKKFEKYRLKQIMDNIYKGKIIEINKMKN
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ISQQ IGCSFGCCKFCATGQIGIKRQLDI DEITPOLLYFOSKOVDIKNI SFMGMGEPLAN
PYYFDSI OFFUNNILESI SWRRIN ISTVGLLAGIKKLINI FPQVNILAFSLHSPFTERE
DQLVPINKLFPFNEVFDLLDERIAKTGRRWISYILLIKNINDSKOHABALSDHI CKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 254449)
Gardner,M.J.
Direct Submission
Submitted (13-55P-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2707,2795. .>2856)
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join(<1089. 2095,2658. .2707,2795. .>2856
form(1089. .2095,2658. .2707,2795. .2856)
join(1089. .2095,2658. .2707,2795. .2856)
/locus_tag="PP14_0066"
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/isolate="3D7"
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locus tag="PF14_0067"
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DICHTRALIDLINTNNINKLLQNKYOJFKVRCPONCHNSFRALIEGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTIFBGSTI
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KYDPYNDIALLILILILETERKEIERKESMOKIHGNNMEVIKKGNIIYNNMKAVETYF
TKLEDILINKQLKQKYNFTERTEELLKRQMYECKKLSNYDEIKNTYVVNFND
IKNKPKLNSKKKYMFICIYILEREIEV"
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KFGQTYHISLVFNKINKTLYLYINGKKVITEKNTYNPTLSGDLIIGRSNQTTKDYFIG
NIHLVEIYKYTLSEQEIKESLNSSLSLEYLNMILEQMSNTKKDKKKNQKNKKGVQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDGRDCVTPCKSKNMINKDLQINTQQINLKCQDNLLSEQFNGKIGSQF.VSCIENČTK
KYF IKGNINYYTPDSSICKAAIHAĞIYKPNMGNNYPTRIKVBGLEYKSSKGHFG
ILSKSEKĞQSQLRSEVUSRNERNIFUCSTDQQFILMLSVGEKRTINCPSNCNIIKDKI
YGTNIYSPTSVLCKAAIHSGALSNQGGLVEIIVGTGQEFKGSTQNNVESFSSNNHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLSVATTGDVFLASCPEKCDEEVGIVKGTFLYTYDSPICKSAIHSGVLPNNIAEDIVL
SIAHTHNNFIGTKRNNIESHDFKGTSKSFTISIPTMSLLREERKSNPKSEDEMINKNB
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                                                                                                                            IGNPEYIHIKLNSQNKNWKCKKITVWKDYKYWVPDCIGSLNDKKPESTYFLSGNKIYI
AYVQTGKDIEAATTGTIEIILLGNNKRSNTKVLHEGFSAGGLKKIKFQASDVGELEDI
                                                                                         DSISRYMIETIPILSKDVDLYSNVSLVLSNGYGSKTKEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="fibrillarin, putative"
protein_id="AAN36680.1"
db_xref="G1:23497132"
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protein_id="AAN36681.1"
db_xref="G1:23497133"
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complement(11566, ->12129)
/locus_tag="pF14 0069"
complement(11566, .12129)
/locus_tag="pF14_0069"
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'Trpt type=tandem

9180. .9281

/rpt_type=tandem

9188. .9282

/rpt_type=tandem

10250. .10291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt type=tandem
1060. .11095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
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mRNA

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cli433. .>17104
locus tag="PP14 0070"

join(44433. .15182,15308. .15394,15575. .15704,15867. .16008,
16141. .>17104)
locus tag="PP14 0070"
locus tag="PP14 0070"
join(14433. .15182,15308. .15394,15575. .15704,15867. .16008,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162655 GATGATGATAATGTAGATGATGATAATGTAAATGCTGATAATGTATATGTTGATAATGTA 162596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162595 AATGTTGATAATGTAGATGCTGATAATGTAGATGTTGATAATGTTGATAATGTTGATAATGT- 162537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAN36682.1"
/db_xref="G1:23497134"
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YHMNNNNNMFNNTLNSFVNKTGDIISPYHANIHDNSQLTMKYKLGGNIITNNSFHSS
NTNYTNBEKKANCLEMTNTTTYNVNTLLRNNILSSEYPKSLIPIKTFKEVVDEIHSYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVEPYCIGSNRAPSTLFCCLYKFFTMQLSEKQLKSLIENKDSCYIRACGFLYLRYVHS
SHANWAWFRSYLLEBDFS SLGOKRKRYTIGBYQSLLSDNSYKTNTUFRLPIXKAV
YGARLANI IDDHRRELKKYKKNENISKFLKGEPVLAYINGEWEKGBIGGYVNHGNFFYR
LREIDGNIELLVNIGYVKLEGKDSHKEKDIQKHKSRERSTSISERKRRRRRNSSSKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRRKSRHGRSSSRRKRKRRQRDESRSSSRTRRRBHNRSHKRGSSYEKDYSIDKYSSRS
HSRSRRRKHSSKHSSHYKSHNNHRDRSINKYNRPSEEDELYKSKKRRNVSISRSSSS
TRYRKEKYEKTEDELISRPKKLESQKALATGKDYARRPTSYKSSLSLKVDNIPVRRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSRS PRRI DNRVVVQVVHTDNTNNDNNTSENMKLKELMKKYNKDDTNDEPKMNNSNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             754 CCCGAGGCCTATAAAGTCACAGCAGATAGTCTACCTGCCACATTATTAGAAGTGGTTCCA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATCGAAGTATCCAAACCTGCAACATGTTATTGACGCTGTGGGAAGAAGATAGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 CATATCAATGCTTATACTAAGATTGTAACTGTTGCTTCTAAAAAGCATGAAAAGCTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            634 AAGTCTTATGGTGCTGATGATGTCTTTGACTATCATGATGCAGGCGTTATTGAGCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47.4; DB 3; Length 254449;
Pred. No. 2.8;
0; Mismatches 291; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_type=tandem
complement(<18138. .>18722)
/locus_tag="PF14_0071"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="PF14_0070"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15212. .15255
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15247. .15277
/rpt_type=tandem
15275. .15301
                                                                                                                                                               /rpt_type=tandem
13821. .13862
/rpt_type=tandem
14163. .14245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_type=tandem
17274. .17328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_type=tandem
16038. .16117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_type=tandem
17892. .17931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_type=tandem
17929. .17988
                                                  /rpt_type=tandem
12742. .12781
                                                                                                          /rpt_type=tandem
12969. .13026
                                                                                                                                                                                                                                                                             /rpt_type=tandem<14433. .>17104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type=tandem
/rpt_type=tandem
[2512]. .12547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16141. .17104
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Best Local Similarity 44.4%;
Matches 235; Conservative
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5007 TTTTGTTGCTGCTGCTACTGTTGTTGCTGCTGCTACTGTTGTTGCTGCTGCTACTGT 5066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 TGAAGGTGACAAAGCTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1947 recreationereristriciteriscrecrecrecrateristriciteriscrecrecrecrecre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 TAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Destination of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 83922 bases at least Q10
Consensus quality: 83954 bases at least Q20
Consensus quality: 83954 bases at least Q20
Consensus quality: 83954 bases at least Q20
Insert size: 89000; agarose-fp
Insert size: 84018; sum-of-contigs
Quality coverage: 13.13x in Q20 bases; agarose-fp
Quality coverage: 13.13x in Q20 bases; sulse-field-gel
Quality coverage: 13.7x in Q20 bases; sulse-field-gel
Quality coverage: 13.9x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .7443
/note="clone overlaps with GenBank Accession Number AC096997 clone 217A23 (center project name arb)" 11110. .84118
/note="assembly_fragment
order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least RX average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 1100 11109: gap of unknown length 11110 84118: contig of 73009 bp in length 1100 length 1110 and 1100 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 length 1110 le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 230; Indels
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/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db xref="taxon:31033"
/clone="241N7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="Incyte Genomics"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vecto<u>r</u> side:right"
a 2090<u>9</u> c 21005 g 21345 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Neopterygli; Teleostei; Euteleostei; Neoteleostei; Acanthopterygli; Teleostei; Euteleostei; Neoteleostei; Acanthopterygli; Percomorpha; Tetradontiformes; Tetradontoidae; Tetradontoidae; Takifugu.

E 1 (bases 1 to 84118)

S Akther, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carigga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haphighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskerli, B., McDowell, J., Reddix-Dugue, N., Schandider, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                     162418 GTAAATGTTGATAATGTAGATGCTGATAATGTAAATGTTGATAATGTAGATGCTGATAAT 162359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162298 ATTAGTGTTAATAATGTTGATGCTCTTTATAATATTTGGTGTTCATGATGATGATGAT
                                                     162478 GTAGATGTTGATAATGTTGATAATGTAAATGTTGATAATGTTGATAATGTAAATGTTGATAAT 162419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       994 GGTGATATCCATCATATGAATATTAAAGTTTTCAGCAACGGCTTAGATGATGTCCCAGCT 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC096684 84118 bp DNA linear HTG 20-NOV-2002 Takifugu rubripes clone 241N7, WORKING DRAFT SEQUENCE, 2 ordered
                                                                                                                                                                                                                                                                                                                     874 TTGTTGTATCGTGCATCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGT 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934 CCAGAATATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAAC 993
                                                                                                                                          ATGACCATTGAAAGCATTCCTGAAGAATCAGAAAAGATAATGTTAAAATTGATATTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (20-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Nov 20, 2002 this sequence version replaced gi:15721942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (22-SEP-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 84118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162238 GATGACGATGATGATGATGATGATGATGATGATGATGATATGATG 162190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1054 CTCACTGAAGGTATAAAAGAAGGTAAAAACAAAAATGTTAAGTATGTTG 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: NIH Intramural Sequencing Center
        Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC096684.2 GI:25139901
HTG; HTGS PHASE2; HTGS DRAFT.
Takifugu rubripes (Fugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 241N07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: arc
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KEYWORDS
SOURCE
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COMMENT

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5067 IGTICTACTCCTGCTGCTGTTGTTGTTGCTGCTGCTACTGTTGTTGCTGCTGTTGT 5126
                                          216 TGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGG 275
                              276 IGCTICCCAAACAGAICCIAAAAAIGGIGCATTIGCTGAATAIGCCAGGGTTTAICCACC 335
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Search completed: January 10, 2004, 07:53:15 Job time : 4393 secs

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40.2 3.6 439 22 40.2 3.6 439 22 40.2 3.6 439 22 40.2 3.6 439 22	13 40.2 3.6 439 22 14 40.2 3.6 439 22	15 40.2 3.6 439 24 16 40.2 3.6 439 24 17 40 3.6 1236 24 18 39.6 3.6 1050 24	19 39.6 3.6 4027 2.7 AAK5/473 21 39.6 3.6 50000 24 ABL55644 22 39.4 3.5 772 18 AAT91162 22 39.4 3.5 1035 24 ABN66435	23 39.4 3.5 1131 18 24 39.4 3.5 2155561 24 25 38.8 3.5 392 25	38.8 3.5 2365589 24 38.4 3.5 847 20 38.2 3.4 486 22	38 3.4 43576 21 38 3.4 50000 24	37.6 3.4 987 25 37.6 3.4 3073 12	37.6 3.4 640681 24 37.6 3.4 2162598 25	36 37.4 3.4 4920 23 37 37.4 3.4 237961 24	37.2 3.3 860 22 37.2 3.3 1350 23	37.2 3.3 2792 21 37.2 3.3 1163020 24 77.2 3.3 3011208 24	37 3.3 1755 24 37 3.3 1755 24	44 37 3.3 1923 23 45 37 3.3 3582 21 46 37 3.3 7008 22	37 3.3 8772 22 37 3.3 8871 22	49 37 3.3 9121 21 50 37 3.3 9321 24	51 37 3.3 9401 22 52 37 3.3 10531 25	53 37 3.3 11762 25 54 37 3.3 198285 24	55 37 3.3 198285 24 56 37 3.3 910715 20	57 37 3.3 2155561 24 58 36.8 3.3 441 22	59 36.8 3.3 441 22 60 36.8 3.3 441 22	61 36.8 3.3 441 22 62 36.8 3.3 441 22	63 36.8 3.3 441 22 64 36.8 3.3 441 22	36.8 3.3 441 22 36.8 3.3 441 23	67 36.8 3.3 441 24 68 36.8 3.3 3150 24	59 36.8 3.3 4629 23 70 36.8 3.3 6693 23 71 36 6 3 3	36.6 3.3 2240 23	36.6 3.3 6253 20 36.6 3.3 6253 24 36.6 3.3 1664976 19	36.2 36.2 36.2 36.2 36.3	81 36.2 3.3 580073 18
5.1.6 Compugen Ltd.		; Search time 376 Seconds (without alignments) 7990.624 Million cell updates/sec	agtatgttgccaggttataa 1113		диев	ters: 5105512 .				neseqn-embl/wA1980.DAT:*	q/genesegn-emb1/NA1981.DAT:* qq/genesegn-emb1/NA1982.DAT:* c/genesegn-emb1/NA1983.DAT:*	neseqn.embl/na1984.bar. neseqn.embl/na1984.bar.* neseqn.embl/na1985.bar.*	neseqn.embl/Nal965.DAT:* neseqn.embl/Nal965.DAT:*	neseqn-emb1/NA1988.DAT:* eneseqn-emb1/NA1989.DAT:*	enesegn-embl/NA1990.DAT:* enesegn-embl/NA1991.DAT:*	eneseq. embl/NA1992.DAT:* eneseqembl/NA1993.DAT:*	enesegn-embl/NA1994.DAT:* enesegn-embl/NA1995.DAT:*	enesegn-embl/NA1996.DAT:* enesegn-embl/NA1997.DAT:*	enesegn-embl/NA1998.DAT:* enesegn-embl/NA1999.DAT:*	enesegn-embl/NA2000.DAT:* enesegn-embl/NA2001A.DAT:*	genesegn-embl/NA2001B.DAT:* genesegn-embl/NA2002.DAT:*	enesegn-embl/NA2003.DAT:*	predicted by chance to have a score of the result being printed,	score distribution.		Description	S. cerevisiae BAX- Human ORFX polynuc C. albicans BAX-as	Staphylococus aur Staphylococus aur Plaemodium falcipa Human breast cell	Human foetal liver
GenCore version Copyright (c) 1993 - 2004	OM nucleic - nucleic search, using sw model	Run on: January 10, 2004, 05:08:13 ; (w	Title: US-10-081-644-1 Perfect score: 1113 Sequence: 1 atgtcagttccaaccactca	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	hed: 25527	mper o	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100%	first	Geneseg 19Jun03:* /SIDS1/gcgdata/genese	data/genese data/genese data/genese	/SIDS1/gcgdata/genese /SIDS1/gcgdata/genese /SIDS1/gcgdata/genese	/SIDS1/gcgdata/genese /SIDS1/gcgdata/genese /SIDS1/gcgdata/genese	/SIDS1/gcgdata/genese/SIDS1/gcgdata/genese	/SIDS1/gcgdata/genes /SIDS1/gcgdata/genes	/SIDS1/gcgdata/genee /SIDS1/gcgdata/genee	/SIDS1/gcgdata/gener	/SIDS1/gcgdata/gener /SIDS1/gcgdata/gener	/SIDS1/gcgdata/gener /SIDS1/gcgdata/gener	/SIDS1/gcgdata/gener   /SIDS1/gcgdata/gener	/SIDS1/gcgdata/gener /SIDS1/gcgdata/gener	25: /SIDS1/gcgdata/gene	No. is the number of results greater than or equal to the	derived by analysis of the		No. Score Match Length DB ID	357	4.1 23439 14 AAV74 3.7 3501 21 AAA77 3.6 439 22 ABA49	8 40.2 3.6 439 22 ABA67

Probe #13320 for g Human brain axpres Human brain axpres Human brain axpres Human brain axpres Human ilver single Human immuns/haema Amby genome fragm Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Strawberry fruit a Straptococcus poly Straptococcus poly Straptococcus poly Human CDNA differe Gustall a hungdorfe Streptococcus poly Human REPTR 9 cDNA Human REPTR 9 cDNA Human GDNA differe Gene #3317 used to Borrella burgdorfe Streptococcus poly Human brasin axpres Human brasin axpres Human brasin axpres Human brasin axpres Human liver single Human liver single Human liver single Human denome-dariv Arabidopsis a hallanog Brosophila melanog Brosophila melanog

Enterococcus faeca Enterococcus faeca Methanococcus jann Sequence encoding Bacteriophage 3A c Arabidopsis thalia Nucleic acid seque Mycoplasma genital

Bax gene

This sequence represents a polynucleotide associated with the described in the disclosure of the invention.

Sequence 1631 BP; 477 A; 357 C; 346 G; 451 T; 0 other;

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Gaps

9;

Indels

Score 357.8; DB 24; Pred. No. 2.5e-87; 0; Mismatches 452;

32.1%; 58.8%;

Local Similarity 58.8 Les 658; Conservative

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Query Match

88833

DB 24; Length 1631;

63

4 TCAGTTCCAACCACTCAAAAAGCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACA

510 regarrecagaaaceargaaageegrrerearrgaaaaregeaageererageaa GATGTCTCAGTTCCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGCT

123 629 GGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTA 183

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630 GGTAACCCTACCGATTGGAACATATTGATTTCAAGATTGGTCCTCAAGGTGCCCTCTTA 689

GGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTG----ACTTG

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414 929

690 GGCTGTGATGCAGCCGGCCAAATCGTAAAGTTGGGCCCAAATGTTGATGCTGCACGCTTT 749

750 GCCATTGGTGATTACATTTATGGGGTTATTCACGGTGCTTCAGTGAGGTTCCCCTCAAAC 809

241 AAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAAT

GGTGCATTTGCTGAATATGCCAGGGTTTATCCACCTTTGTTTTACAA-----GAGTAAC

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Shrimp polynucleot	Haemophilus influe	CFE 98 coding sequ	DNA transcription	Human angiogenesis	Arabidopsis thalia	Haemophilus influe	Staphylococcus aur	S. aureus spood2 p
ABN81097	AAS53374	AAH90794	ABK28448	ABQ67150	AAF22305	AAT42063	AA221567	AAX29297
	~	N	<#	₹#	7	17	20	70
222	312	978	9095	40324	1082138	1830121	840	840
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36	36	36	36	36	36	36	35.8	35.8
82	83	84	82	98	87	88	83	90
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## ALIGNMENTS

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Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss.
                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                Reekmans RJ
                                                                                    cerevisiae BAX-associated cDNA fragment SEQ ID 331
                                                                                                                                                                                                                                                                                                               Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 36; Figure 1; 344pp; English
                     ABQ76453 standard; cDNA; 1631
                                                                                                                                                                                                                                               22-DEC-2000; 2000EP-087031B.
04-JAN-2001; 2001EP-0870002.
09-JAN-2001; 2001EP-0870003.
                                                                                                                                                                                                                                                                                                               Contreras RH, Eberhardt I,
                                                                                                                                                                                                                            21-DEC-2001; 2001WO-EP15398
                                                               (first entry
                                                                                                                                                              Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                          (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                    WPI; 2002-667002/71.
                                                                                                                                                                                                                                                                                                                                                                                                     certain diseases
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                                           ABQ76453
RESULT 1
            ABQ7645
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1050 GCCACTGCTGTTGGCCAGATGCTTATTCAATTGGCAAAAAACTTAAACGGTTTCAGCAAG 1109
                                                                                                                                                                                                               1110 ATCATCGTCGTTGCTTCTCGTAAACATGAAAATTGTTGAAAGAGTACGGTGCAGATGAA 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1230 CCTTACTTGGTGGACTGTGTCTCCAACACAGAAACTATTCAACAGGTGTACAAATGTGCC 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1290 déridatearriadacécracerrerrearricacerritaaceanaaadarareng 1349
                                                                                                                                                                                                                                                                                                                                                                                                                          1170 CTTTTTGACTACCACGATGCTGACGTTATCGAACAGATAAAAAAGAAGTACAACAACATT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1410 AACGACGTCCCATTTGGCACGTTTACTTTGCCAGCAGACCCTGAATACAAGGAAGCCGCC 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895 CAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACA 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          835 GAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTGTTGTATCGTGCATCTGGT
                                                                                                                                                                                                                                                                                                                     655 GTCTTTGACTATCATGATGCAGGCGTTATTGAGCAGATCAAATCGAAGTATCCAAACCTG
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                                                                                                               ATTGTAACTGTTGCTTCTAAAAAGCATGAAAAGCTTTTAAAGTCTTATGGTGCTGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACATGTTATTGACGCTGTGGGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACA
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                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fund; identifying, or obtaining and identifying candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death. The products of the invention have cytostatic, fundicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cytostatic, fundicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cytostatic, fundicide; pharmaceutical compositions, antisense molecies and antibodies are useful as medicament for reacting, preventing and/or alleviating diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and preparing a medicament for modifying the endogenic flora of humans and cher mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, ischaemia, diseases related with viral infections or neurodegenerations.
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GCTACAGCAGTGGGTCAACAACTAATCCAAGTTGCCAAACATATCAATGCTTATACTAAG

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415 GCATCATTGCCAGTTTCGTTGACAACTGCTGGTGTTAGTTTGTGTCATCACTTGGGCTCA 474

930 GTATCCCTCCCAGTCTCATTGACCACGGCTGGTATGATCCTTACACATAGTTTTGGCTTG

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475 AAAATGGAATGGCACCCATCTACCCCGCAACATACTCCATTATTGATTTGGGGTGGT 990 GACATGACATGGAAGCCCTCCAAAGCGCAAAGAGATCAACCCATCTTATTTTGGGGTGGT

355 TTAACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1)

In the specification). ABN15762 to ABN27252 encode the human ORFX

proteins given in ABP00010 to ABP11500. ORFX proteins are useful for

treating or preventing a pathology associated with an ORFX-associated

disorder in humans, and in the manufacture of a medicament for treating a

cyndrome associated with ORFX-associated disorder. ORFX polymucleoride

squances can be used in gene therapy. ORFX sequences can be used in the

treatment of cancer, hyperproliferative disorders, cirrhosis of liver,

psoriatists, benign tumours, keloid, degenerative disorders related to organ

transplantation, cardiovascular diseases, diabetes mellitus, systemic

lupus srythematosus, hypertension, hypothyroidism, cholesterol ester

storage disease, various immune deficiencies and disorders, infacettous

diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host

disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                 GITAAATICGITAAGITITATAAATCCACACCTIAACAACGGIGATATCCATCATATGAAT 1014
                                                                                                ATTANAGITTTCAGCAACGGCTTAGATGATGTCCCAGCTCTCACTGAAGGTATAAAAGAA 1074
                                                                                                                                            Greanactrinachagancecerrachrearacceacherracricarchrantaneche 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                  GGTAAAAACAAAATGTTAAGTATGTTGCCAGGTTATAA 1113
                                                                                                                                                                                                                                                 GGGAGGAATTCTGGCGAAAGTTGGTTGCCGTCTTGAAA 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX polynucleotide sequence SEQ ID NO:21835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 21835; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                        ABN26679 standard; cDNA; 393 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myasthenia gravis; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-106308/14.
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ABN ASS 6579

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 GAACTTCGAATCTGCTGCATCATTGCCAGTTTCGTTGACAACTGCTGGTGTTAGTTTGTG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 ATTGATTTGGGGTGGTGCTACAGCAGTGGGTCAACAACTAATCCAAGTTGCCAAACATAT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GAGGTTCCCCTCAAACGGTGCCTTTGCTGAGTACTCTGCCATTTCATCCGAGACTGCTTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 TAAACCAGCCAGAGAGFTTAGATTGFGCGGTAAAGACAAGCTACCAGAAGGCCCCGTAAA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 ATCTTTAGAAGGGGCAGTATCCCTCCCAGTCTCATTGACCACGCCTGGTATGATCCTTAC 251
                                                                                                                                                                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; se.
useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative discorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 réargerecacecrirecearrégigarracarriangeserrarredécerécricaer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 ACATAGTTTTGGCTTGGACATGACATGGAAGCCCTCCAAAGCGCAAAGAGATTCAACCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 AACAGATCCTAAAAATGGTGCATTTGCTGAATATGCCAGGGTTTATCCACCTTTGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA-----GAGTAACTTAACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATCACTTGGGCTCAAAAATGGAATGGCACCCATCTACCCCGCAACATACTCATCTT
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9
                                                                                                                                                                                                                                                                                                                                                                                                      Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels

    C. albicans BAX-associated cDNA fragment SEQ ID 557.

                                                                                                                                                                                                                                                                                                                               Sequence 393 BP; 101 A; 93 C; 91 G; 107 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                              8.8%; Score 98.4; DB 24;
55.8%; Pred. No. 9.1e-17;
ive 0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACGGTTTCAGCAAGAT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ76566 standard; cDNA; 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-2000; 2000EP-0870318.
04-JAN-2001; 2001EP-0870002.
09-JAN-2001; 2001EP-0870003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-2001; 2001WO-EP15398.
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                                                                                                                                              systemic cytokine damage.
N.B. The sequence data f
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.8
Matches 211, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans.
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485 GTATTTTGATTTTGGGGGAGGAACTGCAACTGGAGTTCTAGCCATTCAGGTTGCCAAAC 544

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This invention describes a novel nucleic acid representing a synthetic.

Bax gene. The Bax gene of the invention is useful for identifying and identifying candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cytostatic, fungicide; pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alleviating a scancer, or for preventing applyers in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preventing applyers, in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preventing apportosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preventing and infections and infections Apoptosis-related diseases include autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polynucleotide associated with the Bax gene described in the disclosure of the invention.
                                                                                                                               New isolated nucleic acid representing a synthetic Bax gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases
  Reekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1086 BP; 359 A; 174 C; 223 G; 330 T; 0 other;
  Luyten WHML,
                                                                                                                                                                                                                                                                       Claim 36; Figure 2; 344pp; English
  H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.48;
  Eberhardt
                                                 WPI; 2002-667002/71.
P-PSDB; ABG93300.
  Contreras RH,
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27; Gaps Score 71; DB 24; Length 1086; Pred. No. 4.2e-09; 0; Mismatches 310; Indels 27 49.08; Ouery Match Best Local Similarity 49.0 Matches 324; Conservative

454 154 AAATAİTAAİCAAAGCAĞTAĞCİTITİĞCAATAAACCCAACİĞAİTĞĞAAĞGÇACAİTĞTİT 148 ATAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAAC 214 ATCAATTGGGCAGCCCAGGTGATGTTGTTGGTTGCGATGTTAGTGGGATCATTGAAGAAG 208 TTGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACG 274 GTGCTTCCCAAACAGATCCTAAAAATGGTGCATTTGCTGAATATGCCAGGGTTTATCCAC 334 Gra-----Aradarcaccrccacacrcsadcrrrrscagaararcracrcrarcrc 319 CTACTTCGATAAAGTACAATAAGAATTTTGAACATTTGACTAATTTACAAGTATCTGAAA 379 TCCACTCATTTGAAGGGGCCAGCAAGTATTAAATTTAGGTTTGGGTTACCGTTGGGCTTTTCAT 439 574 CTITIGITITACAAGAGTAACTTAACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCTG 394 TGTGTCATCACTTGGGCTCAAAATGGAATGGCACCCATCTACCCCGCAACATACTCATC 514 TTTCTCATTACTTACGAATTGACAACAAAAGCAACC--------TGGGGGATA 484 CATTATTGATTTGGGGTGGTGCTACAGCAGTGGGTCAACTAATCCAAGTTGCCAAAC CAGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCCAACTGATTGGAAGCATATTGCTT TTGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTA TGAAGAACTTCGAATCTGCTGCATCATTGCCAGTTTCGTTGACAACTGCTGGTGTTAGTT 95 149 380 29 83 155 215 209 275 266 335 320 455 440 원 ò 셤 g g ò 윱 g ò g ઠ ò 셤 ò ò 8

634 694 Yeast, protein-protein interaction, Selected Interacting Domain; SID (RTM); secretion yield, cancer, neurodegenerative disease, fungicide; cytostatic, neuroprotective, gene, ds. 954 601 661 9 The present invention relates to complexes between Saccharomyces cerevisiae Selected Interacting Domain (SID (RTM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that modulate the interaction of proteins, for developing yeast strains with better secretion yield of protein, and in gene therapy. The protein complexes, polypeptides and polynucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present sequence is a coding sequence of the invention. New protein-protein complexes of Saccharomyces cerevisiae, useful in drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida 602 AACAATTAGGGGCAGATTATGTTTTTCGATTATGGAGACGCTGATGTTGTCAATAAAATTA 575 ATATCAATGCTTATACTAAGATTGTAACTGTTGCTTCTAAAAAGCATGAAAAGCTTTTAA 545 TAGTGTA---TAATCTCAAAGTAATCACCACAGCATCACCCAAAAACCACACACCTTGA 635 AGTCTTATGGTGCTGATGATGTCTTTGACTATCATGATGCAGGCGTTATTGAGCAGATCA 895 CAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACA 1 cargaagraccarrregaaacarracrrraccagccgacrcagaagcraggaaagcrgca Yeast selected interacting domain coding sequence SEQ ID NO: 15. ö 5.8%; Score 64.4; DB 24; Length 1330; llarity 56.0%; Pred. No. 2.9e-07; Conservative 0; Mismatches 96; Indels 0; Sequence 1330 BP; 420 A; 257 C; 207 G; 446 T; 0 other; Claim 7; Page 41; 357pp; English. ABT11258 standard; DNA; 1330 BP 16-FEB-2001; 2001US-269266P. 14-FEB-2002; 2002WO-EP02299 (first entry) Saccharomyces cerevisiae infection or cancer) WPI; 2002-674913/72. (HYBR-) HYBRIGENICS Local Similarity es 122; Conserv P-PSDB; ABJ10941 WO200266504-A2. 695 A 695 662 10-DEC-2002 29-AUG-2002 4 Legrain P; 662 ABT11258; Query Match Best Loca Matches ò g ò g ò 셤 ò

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misc_feature
                                                            misc_f
  /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence "/*tag= b /*tag= "these hare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence...7740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence".11340
GTTAAATTCGTTAAGTTTATAAATCCACACCCTTAACAACGGTGATATCCATCATATGAAT 1014
                                      ATTAAAGTTTTCAGCAACGGCTTAGATGATGTCCCAGCTCTCACTGAAGGTATAAAAGAA 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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                                                                                                                                                                                                                                                                                                                                                                                             "these bases represent a line of missing text in the sequence listing in the specification. They are included maintain the nucleotide numbering given in the specification for this DNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                        GrahGGGrcrarangahCGGGCrrrGrGarGrrCcrcarariccraaaagaCarcaaarar 180
                                                                                                                                                                                                                               Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
            GGTAAAAACAAAATGTTAAGTATGTTGCCAGGTTATA 1112
                                                                                                GGTAAGAACTCTGGTGAAAACTCGTTGCCGTATTAAA 218
                                                                                                                                                                                                             Staphylococcus aureus contig SEQ ID #38.
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
481..540
/*tag= a
                                                                                                                                                   ВР
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anti-S.aureus vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15958 ACCTGTTTTCATTGCGCATTGTAATGGCGATTATGATGTTCCCGTTGAGGAAAGCGAACA 15899
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                                                                                                                                                                                                                                                                                                                                                                         564 AGTTGCCAAACATATCAATGCTTATACTAAGATTGTAACTGTTGCTTCTAAAAAGCATGA 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 AGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTAAAA 862
                                                                                                                                                                                                                                                                         504 ACATACTCATCCATTATTGATTTGGGGTGGTGCTACAGCAGTGGGTCAACAACTAATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAGCTTTTAAAGTCTTATGGTGCTGATGATGTCTTTGACTATCATGATGCAGGCGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:335.
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                                                                                                                                                                                                                          Gaps
(and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.
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                                                                                                                                                                      DB 18; Length 23439;
                                                                                                                                                                                                                       ö
                                                                                                                       789 other;
                                                                                                                                                                 Query Match 4.1%; Score 45.4; DB 18; Length Best Local Similarity 45.4%; Pred. No. 0.14; Matches 163; Conservative 0; Mismatches 196; Indels
                                                                                                                     Sequence 23439 BP; 7768 A; 3506 C; 4455 G; 6921 T;
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of furgs to treat or prevent P. falciparum prince in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of for plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite biology, a process hampered for vaccine and drug development. Parasite resistance to drugs and mosquito resistance of insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB181352 represent nucleotide and protein sequences given in the present invention, but which are not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specifically mentioned within the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid probes for measuring gene expression in a sample derived the probes with a collection of detectably labelled nucleic acids derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the coxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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46.8%; Pred. No. 0.74;
tive 0; Mismatches 143; Indels 0
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
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Matches 126; Conservative
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                                            WO200157271-A2.
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                                                                                                                                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 0.74;
0; Mismatches 143; Indels 0
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                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #16101.
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ABA67796 standard; DNA; 439
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2000US-0608408
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Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, disgnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 AGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTA 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 TGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 TGATGGTGGTGATGGTGATGCTGCTGCTGATGATGGTGGGGGATAATGATGGTGGTGC
                                                                                                                                                Probe #13320 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                      Human; gene expression; heart; microarray; vascular system; probe;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40.2; DB 22; Length
Pred. No. 0.74;
0; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 439 BP; 141 A; 169 C; 41 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                     reargargeraargargargerg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID No 13320; 530pp; English.
TGCTTCCCAAACAGATCCTAAAAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR
                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                            congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%;
                                                                                                                                                                                                                                                                                                                                            2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0608408.
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                                                                             ABA34854 standard; DNA; 439
                                                                                                                                                                                                                                                                                                                                                                             2000GB-0024263
                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                            03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000;
                                                                                                                                                                                                                   Homo sapiens
                                                                                                                          23-JAN-2002
                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                   ABA34854;
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                                                                   ABA34854/c
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                                                                                                                                                                   205 TCCTGCTGATGGTTTTGATGGTTGATGGTGATGCTGCTGACGGTGATGGTGATGGTGA 146
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156 TAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 TGATGGTGGTGATGCTGCTGCTGCTGATGATGGTGGGGGATAATGATGATGGTGGC 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
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                                                             265 TGCTGATGGTGATGATGGTGGTGATTACGATGGTGATGCTGCTGCTGCTGCTGCTGGTGA
                                                                                                                             TGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe SEQ ID NO: 16198.
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0.74:
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                                                                                                                                                                                                                                                               TGCTTCCCAAACAGATCCTAAAAATGGTG 304
                                                                                                                                                                                                                                                                                                                            Score 40.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
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26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
33-AUG-2000; 2000US-053386.
21-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK16207 standard; DNA; 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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Matches 126; Conservative
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96 AGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTA 155
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                                                                                                                                                                                                                                                                                                                              12-OCT-2001
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                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                   AAI22718;
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TGCTGATGGTGATGATGGTGATTACGATGGTGATGCTGCTGCTGCTGCTGGTGTGA 206
                                                                                                 TGGACCAAATGCTAGTACTGAACGTTGGAGATACCGGTTTCGGTTTTGTTCACGG 275
                                                                                                                             TCCTGCTGATGGTTTTGATGGTTATGATGATGGTGCTGCTGCTGACGGTGATGGTGA 146
                                           TAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACT
                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 16510; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO: 16510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%; Score 40.2; DB 22; Length 439;
llarity 46.8%; Pred. No. 0.74;
Conservative 0; Mismatches 143; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 439 BP; 141 A; 169 C; 41 G; 88 T; 0 other;
                                                                                                                                                       TGCTTCCCAAACAGATCCTAAAAATGGTG 304
                                                                                                                                                                                  145 reargargargarargargargarg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
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26-MAY-2000; 2000US-0207456.
30-UJN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0234687.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                           953/c
AAK41953 standard; DNA; 439
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                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                              06-NOV-2001
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                         Probe #12651 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates to human single exon nucleic acid probes
325 TGCCGATGGTGATGGTGATGATGATGGTGATGCTGCTGATGGTGTTGATGGCGATGC
                                  156 TAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACT
                                                                   216 TGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGG
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analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 439 BP; 141 A; 169 C; 41 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                           TGCTTCCCAAACAGATCCTAAAAATGGTG 304
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2000US-0608408.
2000US-0632366.
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Best Local Similarity 46.8
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157278-A2
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03-AUG-2000;
21-SEP-2000;
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385 TGATGGTGGTGATGCTGCTGCTGTTGATGATGCTGGGGATAATGATGATGATGC 326

36 TGAAGGTGACAAAGCTGTTGATAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTAC 95

Similarity

Matches 126;

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TGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGTAC

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                                               TGATGGTGGTGATGGTGATGCTGCTGCTGATGATGATGGTGGGGAATAATGATGATGGTGGTGC 326
                                                                                                    AGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTA 155
                                                                                                                                                      TGCCGATGGTGATGGTGATGATGATGGTGATGCTGCTGATGGTGTGATGGCGATGC 266
                                                                                                                                                                                                                                                                                                                                                                      205 rccrgcrgarggrrrrgarggrrangargargargargcrgcrgacggrgargarggrang
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TGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 439 BP; 141 A; 169 C; 41 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                              276 TGCTTCCCAAACAGATCCTAAAATGGTG
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2000US-0608408.
2000US-0632366.
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2000US-0236359.
2000GB-0024263.
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
03-AUG-2000;
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast third properties of development, inflammatory diseases non-carcinoma tumours.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
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27-SEP-2000;
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3.6%; Score 40.2; DB 22; Length 439; 46.8%; Pred. No. 0.74; ive 0; Mismatches 143; Indels 0

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96 AGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGGATTGGAAGCATATTGCTTA 155
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                          specification for complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipporteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS31005 represent human liver single exon nucleic acid probes of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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       comprising one of 13109 defined nucleotide sequences
                                                                                                                                                                                                                                                                                                                                   Sequence 439 BP; 141 A; 169 C; 41 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 40.2; DB 23;
16.8%; Pred. No. 0.74;
1ve 0; Mismatches 143;
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specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
                                                                                                                              Score 40.2; DB 22; Length 439;
Pred. No. 0.74;
0; Mismatches 143; Indels 0
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                                                                            Sequence 439 BP; 141 A; 169 C; 41 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human liver single exon probe, SEQ ID No 16548.
                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTTCCCAAACAGATCCTAAAAATGGTG 304
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                                                                                                                              3.6%;
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26-WAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
31-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
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Best Local Similarity 46.8
Matches 126; Conservative
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21-SEP-2000; 2
27-SEP-2000; 2
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acide derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acide derived from human lung the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detectably specific hybridisation of detectably labeled nucleic acide from eukaryote; lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; sasigning exons from genomic sequence by the method above mentioned in the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays should be assigned to a single exon pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single exon pattern of expression nallysis, and for the strong in agency particularly expression nallysis, and for identifying exons in a gene, appetite comprising one of 12011 sequences, mentioned in the specification, or encoded by the expression nallysis, and for identifying exons in a gene, pattern of expression analysis, and contact, chondis symment of indentifying exons in a gene, pattern by interstitial lung disease (ILD), familial identify the expression pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystit pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon
                                                                                                                                                                                                                                               Spatially-addressable set of single exon nucleic acid probes, used
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Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
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                                                                                                                                                                                                                                                                              measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID No 15971; 634pp; English.
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                                                                                                                                       Chen W, Rank DR;
                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
27-SEP-2000; 2000US-236359P. 04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                            WPI; 2002-114183/15.
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The present invention relates to novel screening methods for identifying therapeutic agents for diseases associated with protein misfolding. The method involves contacting a yeast cell with a candidate compound, where the yeast cell expresses a polypeptide comprising a misfolded disease protein, contacting the yeast cell with a toxicity inducing agent and protein, contacting the yeast cell with a toxicity inducing agent and candidate compound is a candidate therapeutic agent. The method is useful to screen for therapeutic agents for diseases associated with protein misfolding such as Alzhaimer's diseases (AD), Parkinson's disease (PD), Familial amyloid polyneuropathy, tauopathies (e.g. Pick disease) contactington's diseases, spinocerebellar ataxia (SCA), fragile-X syndrome, myotonic dystrophy, dentacorubral pallidoluysian atrophy (DRPLA) and prion diseases (e.g. Creutzfeldt-Jacob disease (CD)), fatal familia
                                                                                                                                                                                                                                                                                                                  Human; protein misfolding; Alzheimer's disease; AD; Parkinson's disease; PD; Familial amyloid polyneuropathy; tauopathy; frontotemporal dementia; Pick disease; lobar atrophy; trinucleotide disease; fragile-X syndrome; Huntington's disease; spinocerebellar ataxia; SCA; myotonic dystrophy; Gentatorubral pallidoluysian atrophy; DRPLA; Creutzfeldt-Jacob disease; CUD; prion disease; Gestmann-Straussler-Scheinker disease; SSS, FEI; fatal familia insomnia; mad cow disease; scrapie; kuru; anticonvulant; nootropic; neuroprotective; cerebroprotective; htQl03 protein; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for therapeutic agents for protein misfolding disease, by contacting a yeast cell with compound, that expresses misfolded disease protein, and with a toxicity inducing agent, and evaluating cell for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "Human htQ103 protein"
                                                                                                                                                                                                                                                                              Human huntington (htQ103) protein encoding DNA.
  TGCTTCCCAAACAGATCCTAAAAATGGTG 304
                                         ricaricaricaratraricaricaricario 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                 AAD44410 standard; DNA; 1236
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P-PSDB; AAE26650.
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insomnia (FPI), Gerstmann-Straussler-Scheinker disease (GSS), mad cow disease, scrapie and kuru). The method is useful for treating a patient with Huntington's disease or Parkinson's disease. The present sequence is a DNA encoding human huntington. (htQ103) protein. This sequence is used to illustrate the method of the invention.
                                                                                                                                                            85 AAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCCAACTGATTGGAAG
                                                                                                                                                                                                                                         GTTGTCAAACTTGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGT
                                                                                                                     25 GCCGTCATCATGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCCAGAGTTCCAGAATTA
                                                                                                                                                                                                  145 CATATIGCTTATAAGATIGGTCCAGAAGGTTCAATICTAGGATGTGACATIGCTGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; viral vector; chromosome mapping; gene mapping; c deficiency disorder; gene; RNA polymerase; ds.
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                                                                               Score 40; DB 24; Length 1236; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a.
/product= "first RNA polymerase (AMV051)"
                                                                                                  0; Mismatches 165; Indels
                                                            Sequence 1236 BP; 368 A; 441 C; 288 G; 139 T; 0 other;
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2000US-0662254
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                                                                                                 Matches 139; Conservative
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                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             comprising a polynucleotide encoding a protein operably linked with a heterologous promoter sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polynucleotide encoding a protein to a vertebrate cell preferably a mammalian cell, such as a human cell. The vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in viron or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy protocols, and for delivering large DNA segments for empineering of vertebrate cells. Polynucleotides of the invention have applications in techniques such as their use as insertion sites for foreign genes of interest, hybridisation probes, for chromosome and gene mapping, in PCR technologies, and in the production of sense or antisense nucleic acids, Vectors of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              provide for stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous polynucleotide inserts which can be delivered in an infected or transformed cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    559 TATTATGAAAAATTTATTATAAAAAACCATTTTCTATGTATAGCAAATATCATGAA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619 GAAAAAGATATTATACTATAGATATAAATATCATTATGATGATATTCCTAAAGAA 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     889 TCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant entomopox virus (BPV) vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed in a stable fraction. The current sequence represents an amsacta moorei entomopoxvirus (AmEPV) first RNA polymerase (AMV051)
                                       polynucleotide encoding protein to vertebrate cell, comprises
polynucleotide encoding protein operably linked with heterologous
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recombinant entomopox virus vector useful for delivering
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0; Mismatches 104;
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Pred. No. 1.
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                                                                                                                                                                                                          Claim 74; Page 245-247; 326pp; English
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Best Local Similarity 49.5
Matches 102; Conservative
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Ruben SM; (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

polynucleotide encoding protein to vertebrate cell, comprises polynucleotide encoding protein operably linked with heterologous

entomopox

recombinant

Novel

promoter sequence

virus vector useful for delivering

Bawden AL;

L1 Y,

Moyer RW,

WPI; 2002-227161/28.

(UYFL ) UNIV FLORIDA

10-AUG-2001; 2001WO-US25287. 10-AUG-2000; 2000US-224479P. 14-SEP-2000; 2000US-0662254.

14-FEB-2002

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                                                             anino acid sequences given in AMM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expression in a patient's genome that affect the activity of (I) by expression in a patient's genome that affect the activity of (I) by expression in active proteins or to supplement the patients own production of (I). Additionally, (I) columnications and polymucleotides may be used to protein of the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic antigen genomic to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAM82169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      819 CATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGATAATTGATATTACTTTGTT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879 GTATCGTGCATCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGA 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             939 ATATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGA 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 TTATGGTGCTGATGATGTCTTTGACTATCATGATGCAGGCGTTATTGAGCAGATCAAATC 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 GGCCTATAAAGTCACAGCAGATAGTCTACCTGCCACATTATTAGAAGTGGTTCCAATGAC 818
                                                                                                                                                                                                                                                                                                                                  represent sequences used in the exemplification of the present invention.
                                                  NAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               699 GAAGTATCCAAACCTGCAACATGTTATTGACGCTGTGGGAAGCGAAGATAGTATCCCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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genetic deficiency disorder; ds.
                Disclosure; SEQ ID NO 22285; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.6%; Score 39.6; DB 22; Length 4027; Best Local Similarity 44.0%; Pred. No. 2.7; Matches 168; Conservative 0; Mismatches 214; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 4027 BP; 1247 A; 875 C; 797 G; 1108 T; 0 other;
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The invention relates to a recombinant entomopox virus (BPV) vector, comprising a polynucleotide encoding a protein operably linked with a heteracologus promoter sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polynucleotide encoding a protein to a vertebrate cell preferably a mammalian cell, such as a human cell. The vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in viron or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy proteocls, and for delivering large DNA segments for engineering of vertebrate cells. Polynucleotides of the invention have applications in techniques such as their use as insertion sites for foreign genes of interest, hybridisation production of sense or antisense mucleic acide. Vectors of the invention provide for stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous polynucleotide construction and expression of the transformed cell and expressed in a stable fraction. The current sequence represents a moorei fragment of the genome of the genus B entomopoxvirus from ameacts moorei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1559 GAAAAAGATATTATACTATAGATATAAGATATAATCATTATGATGATATTCCTAAAGAA 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50000 BP; 20514 A; 4505 C; 4614 G; 20367 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 39.6; DB 24;
49.5%; Pred. No. 7.5;
artive 0; Mismatches 104;
Disclosure; Page 150-175; 326pp; English.
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Best Local S
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ID AAT9
XX
AC AAT9
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DT 27-M
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Fraser C;

Grandi G,

Masignani V, Margarit Ros YI,

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AAT91136 standard; cDNA; 1151 BP
                                                           27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                     29-OCT-2001; 2001WO-GB04789.
                                                                                                              (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                                                                        WPI; 2002-352536/38.
                                                                                                                                                                                                       P-PSDB; ABP25804
              02-MAY-2002.
                                                                                                                                                                  Tettelin H;
                                                                                                                                                   relford J,
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ID AAT9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 TTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus, GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 Trgarccaagrerererereraaarraaagagarcaggregarcaaggrigtre 198
                                                                                                                                                                                                                                                                                                                                                  This cDNA clone corresponds to a strawberry auxin-related gene that is implicated in fruit ripening-related processes. A claimed vector for use in the genetic transformation of strawberry cells comprises a promoter, a regulation sequence and a transcription termination sequence. The regulation sequence comprises the coding region (or a frament of at least 10 bases) selected from 38 claimed strawberry fruit ripening-related genes (see AAT91126.63) that is aligned in the vector in sense or antisense direction. Phenotypically modified strawberry plants can be generated that have one or more of the following fruit characteristics: improved resistance to damage; longer shelf-life; improved processing characteristics; improved flavour and aroma; and modified colour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                        Fruit ripening; strawberry; auxin-related gene; transgenic plant;
                                                                                                                                                                                                                                                                          Modification of ripening of strawberry fruit - using vectors comprising ripening sequences of e.g. O-methyl transferase, acyl carrier protein, cellulase or cysteine protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.5%; Score 39.4; DB 18; Length 772; 65.2%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 772 BP; 215 A; 154 C; 174 G; 212 T; 17 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus polynucleotide SEQ ID NO 783
Strawberry fruit auxin-related gene
                                                                                                                                                                                                                                                                                                                            Claim 2; Page 57-58; 72pp; English.
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                                                                                                                                                             96GB-0018742.
                                                                                                                                       97WO-GB00178
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                                                              Pragaria x ananassa
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23-JAN-1996;
                                                                                     WO9727295-A1
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ABN66435
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the invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (81), given in the specification. The proteins have antibacterial and antihilammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chaminosasays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 TTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAG 159
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New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1035 BP; 304 A; 175 C; 240 G; 316 T; 0 other;
                                                                                                                                                                                                      Claim 7; Page 3229; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 45.8 Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           This cDNA clone encodes a strawberry auxin-related protein that is implicated in fruit ripening-related processes. It was isolated from a cDNA library of strawberry ripening genes by differential screening using cDNA from fruit receptacle tissue at the ripe and white stages of ripeness, and was identified by homology to sequences in the EMBL database. A claimed vector for use in the genetic transformation of strawberry cells comprises a promoter, a regulation sequence and a transcription termination sequence. The regulation sequence comprises the coding region (or a fragment of at least 10 bases) selected from 38 claimed strawberry fruit ripening related genes (see T91126-63) that is aligned in the vector in sense or antisense direction. Phenotypically modified to strawberry plants can be generated that have one or more of the following fruit characteristics: improved resistance to damage; longer shelf-life; improved processing characteristics; improved colur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAAAAACAGATGTCTCAGAATTAAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                    Fruit ripening; strawberry; auxin-related gene; transgenic plant;
                                                                                                                                                                                                                                                                                                         Modification of ripening of strawberry fruit - using vectors comprising ripening sequences of e.g. O-methyl transferase, acyl carrier protein, cellulase or cysteine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39.4; DB 18; Length 1151;
Pred. No. 1.8;
0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1151 BP; 308 A; 205 C; 292 G; 333 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus polynucleotide SEQ ID NO 10967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
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                                                                                                       Fragaria x ananassa Duch cv. Brighton
                                             Strawberry fruit auxin-related gene.
                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 36-37; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 65.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                   (HORT-) HORTICULTURE RES INT
                                                                                                                                                                                                   96GB-0018742.
96GB-0001330.
                                                                                                                                                                            97WO-GB00178
                       (first entry)
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                                                                                                                                                                            21-JAN-1997;
                       27-MAR-1998
                                                                                                                          WO9727295-A1
                                                                                                                                                                                                   09-SEP-1996;
                                                                                                                                                                                                              23-JAN-1996;
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                                                                                                                                                   31-JUL-1997.
                                                                                                                                                                                                                                                             Manning K;
 AAT91136;
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ABN71527/c
ID ABN71527/c
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AC ABN71
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DT 02-JU
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes). Comprising one of 5481 sequences (61), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a componing (I) is used to detect streptococcus in a cused as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chammatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414490 GGCAAAATGGTTATAACTGATACACCAAAACCAGTCATTGAACAAGAGACAGATGCTGTT 414431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414370 AAACGTGAAAGTGGTTCTTTTGCAGGTCATGAGGCTATTGGTATCGTTGAGGAAGTTGGT 414311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414310 ACTAAAGTAACTGACGTGTCAAAAGGTGATTTTGTTATTGTTCCCTTTACACATGGCTGT 414251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antlinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 TCCCAAACAGATCCTAAAAATGGTGCATTTGCTGAATATGCCAGGGTTTATCCACCT 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAG
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Best Local Similarity 45.8%; Pred. No. 40;
Matches 136; Conservative 0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masignani V, Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 4196-4488; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-2001; 2001WO-GB04789
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(GENO-) INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-352536/38.
                                                                                                                                                                             Streptococcus sp.
                                                                                                                                                                                                                                                        WO200234771-A2.
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648

589 ACTAAGATTGTAACTGTTGCTTCTAAAAAGCATGAAAAGCTTTTAAAGTCTTATGGTGCT

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The invention relates to a composition comprising a human GDP-mannose 4.6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the by the level of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences

C ABXI7942-ABXI7944 and ABXI7947-ABX33116 represent DNA molecules encoding human GM4,6D peptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                             Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; sethem; sepsifusion injury; stroke; inffection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
 414250 GGCCAATGTCCGTCTTGTAAGGCTGGATTTGATGGAAATTGTACAAATCATCAAGCT 414194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.5%; Score 38.8; DB 25; Length 392; 55.1%; Pred. No. 1.7; of Mismatches 62; Indels 0
                                                                                                                                                                                                           Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 392 BP; 107 A; 73 C; 98 G; 114 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1620; 6pp; English.
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                                                                                               BP
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                                                                                               ABX19561 standard; cDNA; 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0878574
                                                                                                                                                                        (first.entry)
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Best Local Similarity
Te; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1996;
                                                                                                                                                                        10-FEB-2003
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1760946 TGCAAAAGAAATCATTGAATTTATTGAAAAAATCCAATTTCTTTTATGAATGGTCAAAA 1760887
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                     163 TCCAAGGTAGCAGCTACTGCTAGCACTAGGAACTGGAACTTTAAGGAATTTGGGAGCT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         831 TCCTGAAGAATCAGAAAGATAATGTTAAATTGATATTACTTTGTTGTATCGTGCATC 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           891 TGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence (ABA9021) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The production helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention is related to a Lactococcus lactis nucleotide
                                                                                                                                                                                                                                                                                                                          Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   published 18-OCT-2001) which is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.5%; Score 38.8; DB 24;
55.1%; Pred. No. 59;
tive 0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlich SD;
                                                                                                                                                                                                                                                                                             Genomic sequence of Lactococcus lactis IL1403.
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                                                                                                                                                                                      ABA90521 standard; DNA; 2365589 BP.
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                                                                                                   GACTGGCCTATTGATTAT 240
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                                                                  649 GATGATGTCTTTGACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000; 2000FR-0004630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lactis and related species
                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 55.1
Matches 76; Conservative
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GGTGGTGCTACAGCAGTGGGTCAACTAATCCAAGTTGCCAAACATATCAATGCTTAT 588 103 GGAGGTGCTGGAGTTGGAACCCATGTTATTCAGCTTGCCAAGCATGTTTATGGAGCA 162

Conservative

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à g 957 TAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCATATGAATAT 1016

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by an ancelack acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer.
                                                                                                                                             Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch
al Similarity 46.6%; Pred. No. 3;
117; Conservative 0; Mismatches 134; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gure A, O'Hare M, Obata Y, Old LJ;
Sahin U, Scanlan MJ, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 847 BP; 281 A; 159 C; 136 G; 263 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 67; Page 557; 787pp; English.
                  AAX39814 standard; DNA; 847 BP.
                                                                                                              Gastric cancer associated gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                     98US-0102322.
97US-0896164.
97US-0061599.
97US-0061765.
97US-0948705.
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                                                                              (first entry)
                                                                                                                                                                             prostate cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gout I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfreundschuh M,
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                           WO9904265-A2
                                                                                                                                                                                                                                                                                                         15-JUL-1998;
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                                                AAX39814;
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AAX39814/
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837 AGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTGTATCGTGCATCTGGTCA 896

Local

Matches

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773 AGAATIGICATIGCATAATIGNGAAATITIATIATAATGATITIGCAAATGGCATICAA AGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACAGT

897

713 TAACATTTAATTGAATTTTGAAGAAGTATTATTTTANTACCCTATAAAATGAATCGAAANT 654

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1017 TAAAGTTTTCAGCAACGCCTTAGATGATGTCCCCAGCTCTCACTGAAGGTATAAAAGAAGG 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method of screening for genes which modulate polyglutamine toxicity using animal models with polyglutamine sequences that cause toxicity in the animal. The model is preferably Drosophila, and toxic polyglutamine sequences include the human and Drosophila heat shock protein 40/HDJ1, tetratricopeptide repeat protein (TPR2) and myeloid leuksemia factor 1 (MLF) genes. The model is useful for identifying treatments for neurodegenerative and proliferative disorders, including Alzheimer's disease, Parkinson's disease, Creutzfeldt-Jacob's disease (CJD), bovine spongiform encephalopathy (BSE), Huntington's disease, Machado-Joseph disease, spinocerebellar atxias, dentatorubropallidoluysian atrophy, Kennedy's disease, stroke, head trauma and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                        Animal model; polyglutamine tract; neurodegenerative disorder; HDJ1; heat shock protein 40; terratricopeptide repeat protein 2; TRR1; stroke; myeloid leukaemia factor 1; MLF; human; fruit fly; Alzheimer's disease; Parkinson's disease; CJD; BSE; Huntington's disease; head trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying genes or other compounds that modulate polyglutamine toxicity, useful for treating Alzheimer's disease, Parkinson's disease and Creutzfeldt-Jakob disease -
653 TATTAAAGTICTITAACATAATTTACTCTTTTAAAAATTACCTGTTCATATTTTGTAAAC
                                                                            593 CCATATTTTTAGCACATTAAAAATGAATGTTTGATATTACAGAATATTCATAACAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 486 BP; 193 A; 164 C; 108 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      Polyglutamine tract coding sequence #2.
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12-AUG-1999; 99US-0148934.
18-JAN-2000; 2000US-0177047.
19-WAY-2000; 2000US-0205720.
                                                                                                                                                                                                                                                      AAF75507 standard; DNA; 486
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DB 21; Length 43576; Indels

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11433 TTATTATCTCAAGTCAATTCAATGCGGATACTATTGATAAAAGTATACAAGATGTTATTA 41492
uncharacterised bacteriophage infects a pathogenic bacterium. The compound active on a target of a bacteriophage inhibitor protein in a bacteria is used to treat or prevent a bacterial infection in an animal.

AAA66243 to AAA69442 and AAB16523 to AAB16554 represent bacteriophage nucleotide and protein sequences which are used in the exemplification of
                                                                                                                                                                                                                                                                     764 ATAAAGTCACAGCAGATAGTCTACCTGCCACATTATTAGAAGTGGTTCCAATGACCATTG
                                                                                                                                                                                                                                                                                                           11253 ATGAAGTTGCATTATATGGTGGCTCAAGTCAATCACAAGACATGTATCAAGATACTGCAT
                                                                                                                                                                                                                                                                                                                                                                                           41313 ACGGTGTTAATGTAGGAAATAATAAAGATTATGGATTATATGTTAAATCACAGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                   884 GTGCATCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11373 ATGACATTGTTCTAGAGATTCATTTAGACGCAGCAGGAGAAAATGCAAGTGGTGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAGCCACACTTAAATTCGTTAAAGTTTATAAATCCACACCTTAACAACGGTGATATCC
                                                                                                                                                                                                                                                                                                                                                   AAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a recombinant entomopox virus (EPV) vector, comprising a polynucleotide encoding a protein operably linked with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jene therapy, viral vector; chromosome mapping; gene mapping; deficiency disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant entomopox virus vector useful for delivering polynucleotide encoding protein to vertebrate cell, comprises polynucleotide encoding protein operably linked with heterologous
                                                                                                                                               Sequence 43576 BP; 16057 A; 6485 C; 8769 G; 12265 T; 0 other;
                                                                                                                                                                                     3.4%; Score 38; DB 21; Lilarity 47.2%; Pred. No. 19; Conservative 0; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 125-150; 326pp; English.
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14-SEP-2000; 2000US-0662254.
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                                                                                                       the present invention.
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                                                                                                                                                                                                                                                AGGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTGACTTGAA 242
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                                                                                                                                                                                                                                                                                                                              GGTTGGAGATACCGGTTTTCGTTTCACGGTGCTTCCCAAACAGATCCTAAAAATGG 302
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    GTCAGTTCCAACCACTCAAAAAGCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAAC
                                                                                    AGATGTCTCAGTTCCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGC
                                                                                                                                                                  TGGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a bacteriophage coding region for treating bacterial infections comprises identifying a nucleic acid encoding a product inhibits bacteria when a bacteriophage infects a bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAACTGCTGATGAAATTTCTGAAGG 389
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28-SEP-1999;
30-SEP-1999;
01-DEC-1999;
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29 AAA68609 RESULT

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beterologous promoter sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polynucleotide encoding a protecting of polynucleotide encoding a protecting of polynucleotide encoding a protecting the vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in viro or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy protocols, and for biologically useful proteins in gene therapy protocols, and for call virologically useful proteins in gene therapy protocols, and for call virologically useful proteins in gene therapy protocols, and for call virologically useful proteins in gene therapy protocols, and for their use as insertion sites for foreign genes of interest, hybridisation to probes, for chromosome and gene mapping, in PCR technologies, and in the production of sense or antisense nucleic acids. Vectors of the invention provide for stable integration and expression of heterologous DNA in host calls, and are adapted for accepting large heterologous polynucleotide inserts which can be delivered in an infected or transformed cell and expressed in a stable fraction. The current sequence represents a capture of the genome of the genus B entomopoxvirus from amsacta moorei
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Sequence 50000 BP; 19857 A; 4373 C; 4222 G; 21548 T; 0 other;

979 CCACACCTTAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAGCAACGGCTTA 1038 859 AAAATTGATATTACTTTGTTGTATCGTGCATCTGGTCAAGAAATTCTATTGGGTGCAACA 918 919 AGATITICCTGCTAGICCAGAATAICAIGAAGCCACAGITAAATICGTTAAGITTATAAAT 978 45273 ACTAATGAAGAAGTATCAGAAGCTGCTAATAAATTAATAAAAAATAATACTTGTAATT 45330 1039 GATGATGTCCCAGCTCTCACTGAAGGTATAAAAGAAGGTAAAAACAAAAATGTTAAGT 1096 ö Query Match
3.4%; Score 38; DB 24; Length 50000;
Best Local Similarity 47.5%; Pred. No. 21;
Matches 113; Conservative 0; Mismatches 125; Indels 0; 셤 유 g ઠ ઠે ò

Search completed: January 10, 2004, 06:40:13 Job time : 403 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	nucleic search, using sw model January 10, 2004, 06:26:03 ; Search t:	(without 5582.493	US-10-081-644-1 1113   atgtcagttccaaccactcaagtat	IDENTITY NUC Gapop 10.0 , Gapext 1.0	569978 segs, 220691566 residues	hits satisfying chosen parameters:	length: 0 length: 200000000	: Minimum Match 0% Maximum Match 100% Listing first 90 summaries	Issued Patents NA:*	/cgn2_6/ptod /cgn2_6/ptod /cgn2_6/ptod /cgn2_6/ptod /cgn2_6/ptod /cgn2_6/ptod	is the number of results prediter than or equal to the score	SUMMARIES		Match Length DB ID	.4 8654 .3 1664976	.3 3255 4	.2 1830121 4	.2 1830121 4	.2 849 4	.2 3312 4	.2 3792 2	2 5234 2	2 5234 3	.2 6722 2 .2 6722 3	1 434 4	3.1 360 4 US-09-702-705-1408	.1 360 4 .1 1044 4	.1 1053 4	1 1347 4	.1 4016 4 US-09
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       ORGANISM: Methanococcus jannaschii
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1 Sequence 1, Application US/08916421B

1 Patent No. 5603729

2 TITLE OF INFORMATION:

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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3.4%; Score 37.6; DB 4; Length 8654;
Best Local Similarity 54.3%; Pred. No. 1.8;
Matches 76; Conservative 0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
CORPUTER: HP Vectra 486/33
COFFWARE: ASCII Text
SOFFWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BICOKES. A. Andere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: BB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 8654 base pairs
TYPE: nucleic acid
STREE nucleic acid
STREE NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5572 AĞĞTİTÇAAÇAĞĞTĞİAÇĞİ 6591
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TOPOLOGY:
US-08-961-527-98
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8 ò 원 ð d

APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowiz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: 200-12-08
FRICH REPLICATION NUMBER: 60/073, 189
FRICH FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SCOTWARE: PRECENTING VET: 2.0
SCOTWARE: PRECENTING VET: 2.0 1311772 TATCACTGGTTCAACAATGGATTTGAAAGTTATTGAACTTTGAAAACTTTAAAAAGTTAT 1311713 1311832 TTTTGAATCTGATAAAGTAGGAGAGATTTTAAATAAAATAGATAAAGATACTCTAGTTAT 1311773 3225 ATAGGTGTTGTATCAACAATAATTCTTGGTTCAATAACTATATCATTATCTAATTGTTCT 3166 3165 raraacaaaaaaacarrrrcercrrcracaarracgaarcaagararaaaarrragac 3106 843 CAGAAAAGATAAATTGATATTACTTTGTTGTATCGTGCATCTGGTCAAGAAAT 902 829 ATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTGTATCGTGCA 888 889 TCTGGTCAAGAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAA 948 723 TATTGACGCTGTGGGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACAGCAGATAG 783 TCTACCTGCCACATTATTAGAAGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAAAT 0; Gaps Query Match 3.3%; Score 36.6; DB 4; Length 1664976; Best Local Similarity 49.7%; Pred. No. 27; Matches 93; Conservative 0; Mismatches 94; Indels 0; Query Match 3.3%; Score 36.2; DB 4; Length 3255; Best Local Similarity 45.8%; Pred. No. 2.9; Matches 125; Conservative 0; Mismatches 148; Indels 0 NAME/KEY: misc_feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t, c, or g US-09-601-198-108/c ; Sequence 108, Application US/09601198 ; Patent No. 6531583 ; GENERAL INFORMATION: ; TYPE: DNA ; ORGANISM: Ureaplasma urealyticum US-09-601-198-108 1311652 TAGGTTG 1311646 903 TCTATIG 909 US-08-916-421B-1 ò 셤 ò g ò 요 ò 8

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844860 GTGTTTGTTGAAGGTATCAACATCATTACTAAACATGAAAAACCAGTTCCTGCATTAGGA 844919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 GAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 GTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAG 87
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J. Craig Verter
J. Craig Verter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.2%; Score 36; DB 4; Length 1830121; Best Local Similarity 51.2%; Pred. No. 39; Matches 84; Conservative 0; Mismatches 80; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     844980 AATCCTAAAACAAATAAAGCTGACCGTGTAGGTTTTAGATTCGA 845023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 ATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
ODPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILLING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REFERENCE/DOCKET NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                        APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <UNKNOWN>
                      OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 9410 Key West Avenue CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
  Dell Pentium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
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COUNTRY: U
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APPLICANT: Frager et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment Patent No. 653773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PRIJABL
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR PILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464202 CAGATTATTGGAAATGGCTACATTGATTAATGACAAATATATAAAGAAAAAGTAAAAGC 464261
949 GCCACAGTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCAT 1008
                                             3105 АТААТАĞСАААААСАТТАААТТТАААТАТĞАТАТТТТТĞААААТĞAAĞATGAGCAAATA 3046
                                                                                             1009 ATGAATATTAAAGTTTTCAGCAACGGCTTAGATGATGTCCCCAGCTCTCACTGAAGGTATA 1068
                                                                                                                                           3045 ATTAAAATTAAAATTAAAGTTGTGGGTGACTTGGGGCAAGCTAAAATAATAATTAAA 2986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAATGTTAAAATTGATATTACTTTGTTGTATCGTGCATCTGGTCAAGAAATTCTATTGGG 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          792 CACATTATTAGAAGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAAATCAGAAAAGA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506591
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: the Macleotide sequence of
; TITLE OF INVENTION: the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 580073;
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                                                                                                                                                                                             1069 AAAGAAGGTAAAAACAAAATGTTAAGTATGTT 1101
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ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%; Score 36.2; Dilarity 56.2%; Pred. No. 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                             , Sequence 1, Application US/08545528D
; Patent No. 6537773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1
SOFWARE: Patentin version 3.1
SEQ ID NO L
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COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 68; Conserv
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US-08-545-528D-1
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Best Local S
Matches 68
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ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 GTCATCATTGAAGGTGACAAAGCTGTTGAAAACAGATGTCTCCAGAATTAAAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.2%; Score 36; DB 4; Length 1830121; Best Local Similarity 51.2%; Pred. No. 39; Matches 84; Conservative 0; Mismatches 80; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                844980 AATCCTAAAACAATAAAGCTGACCGTGTAGGTTTTAGATTCGA 845023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 ATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jaworski, Deborah
APPLICANT: Jaworski, Deborah
APPLICANT: Shilling, Lisa K.
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: spooJ2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: Windows 95
SOFTWARE: FASTESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,771
                        APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/POCKET NUMBER: PB186PLC1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10135
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-042-771-1; Sequence 1, Application US/09042771; Patent No. 6080729; GENERAL INFORMATION:
                                                                                                                                                                                                                                          TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                           TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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Sequence 403, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS PAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 TITACAAGAGTAACTTAACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGA 400
                                                                                                                                                                                                                                                                                                                                                                                                                      281 CCCAAACAGATCCTAAAAATGGTGCATTTGCTGAATATGCCAGGGTTTATCCACCTTTGT 340
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                                                                                                                                                                                                                                                                                                            DB 3; Length 840;
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                           ; 77;
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APPLICATION NATA:

APPLICATION NUMBER: U8/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/01571

FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                       Query Match 3.2%; Score 35.8; Di
Best Local Similarity 51.6%; Pred. No. 2.1;
Matches 82; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 403:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 849 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                           TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLLGY: linear
US-09-042-771-1
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                          TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-107-532A-403
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2773 AAAAACAGTTTCTTTTAAAGACGATGCTATTCATAATTTTAGTTTAAAAATTATCAAAAA 2714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3283 ATTCCCAGCAGTTCTCGAGATATTGCTTTATTAGTCGATGAAACAGTTACCAATCAAGA 3342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          768 AGTCACAGCAGATATCTACCTGCCACATTATTAGAAGTGGTTCCAATGACCATTGAAAG 827
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shen, Xiaoyu
APPLICANT: Avruch, Anthony S.
APPLICANT: Yu, Russell V.
APPLICANT: Yu, Russell V.
APPLICANT: Yu, Russell V.
APPLICANT: Nair, Shamila
TITLE OF INVENTION: ENTEROCOCCAL AMINOACYL-tRNA SYNTHETASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       708 AAACCIGCAACAIGTTATIGACGCIGTGGGAAGCGAAGAIAGIAICCCCGAGGCCIAIAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: I THE PC COMPATIBLE
COMPUTER: DEAD FORM:
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BEOOK, David E.
REGISTRATION NUMBER: 22.592
REFERENCE/DOCKET NUMBER: CP195-08
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F04-04
TELECOMMUNICATION 10F04-04
TELECOMMUNICATION 10F04-04
TELECOMMUNICATION 10F04-04
TELECOMMUNICATION 10F04-04
TELECOMMUNICATION 10F04-04
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TELECOMMUNICATION 10F04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                828 CATTCCTGAAGAATCAGAAAAGATAATGTTAAA 861
                                                        1074 AGGTAAAAACAAAATGTTAAGTATGTTGC 1103
                                                                                                        2713 AACTAATCACCAAATCATTACTAGTGATGC 2684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.6;
Pred. No. 4.
                                                                                                                                                                                                                                       Sequence 7, Application US/08855910
Patent No. 6221640
GENERAL INFORMATION:
APPLICANT: Tao, Jianshi
                                                                                                                                                                                                                                                                                                                Tao, Jianshi
Sassanfar, Mandana
Gallant, Paul L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (781) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.9
Matches 80; Conservative
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1139..3559
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STATE: Massachusetts
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-855-910-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                            RESULT 10
US-08-855-910-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1047 CCCAGCTCTCACTGAAGGTATAAAAGAAGGTAAAAACAAAAATGTTAAGTATGTTGCCAG 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR PLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1999-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2893 TAATGAAGATTTAAAATTTACAACCATCACTTCCTAATACACCAAAGATTGATCATTAGA 2834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954 AGTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCATATGAA 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2833 AATTAATAATATTTCGTTTACAATATTAAACAAAACCAAGTTGATATAAAGATTAAGTT 2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTAAAGTTTTCAGCAACGGCTTAGATGATGTCCCAGCTCTCACTGAAGGTATAAAAGA 1073
                                                                                                                                                                                                                                                                                                                                                                                                                         927 IGCTAGTCCAGAATATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCACACCT 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                723 cccaacgcaaacadaadaaacaacrecrecrecrecracrrerraaaacrerrerrecare 782
                                                                                                                                                                                                                                                                                                                                                                   543 rericcagicerigaigericarraacigaarregrircagiarreaaaacaaaacaaac 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603 İGCİGAİCAAĞIAAACGAAĞCAATÇAAAAAACACACAĞİTGACAAİCCITCATICGGGIA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 reargaccercaaarcerrreraecearercarrecaacaacraegerregarerrrea 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    894 TCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCAC 953
                                                                                                                                                                                                                                                                                                                  867 IATTACTTTGTTGTATCGTGCATCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.6; DB 4; Length 3312; Pred. No. 4.2;
                                                                                                                                                                                                                 Length 849;
                                                                                                                                                                                                                                                             0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 109; Indels
                                                                                                                                                                                                               3.2%; Score 35.6; DB 4; 46.7%; Pred. No. 2.4;
                                                                           NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...849
SEQUENCE DESCRIPTION: SEQ ID NO: 403:
                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09601198
Patent No. 6531583
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.2%;
ilarity 48.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 3312
                                                                                                                                                                                                                                                               Matches 113; Conservative
     DRIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                         US-09-107-532A-403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-601-198-58/c
                                                     FEATURE
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1000 ATCCATCATATGAATATTAAAGTTTTCAGCAACGGCTTAGATGATG 1045
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CLASIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: FR 9203034
FILING DATE: 13-MAR-1992
RICH APPLICATION DATA:
APPLICATION NUMBER: WG FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-992-334-2
                                                                                                                                          US-08-302-752-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2229 ATTGCACGAAATCCTGTAACAATAGAAAGCGTTAGGAACAAGATTAAGCGAAAATTGGGG 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2349 ACTCATGAATCAAAGGACGCTATTGCTAAGAATAAACATATATACGACAAAAAAGATATT 2408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                820 ATTGAAAGCATTCCTGAAGAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTG 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              880 TATCGTGCATCTGGTCAAGAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAA 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             940 TATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGAT 999
                                                                     DB 2; Length 3792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2%; Score 35.6; DB 2; Length 3 llarity 47.3%; Pred. No. 4.5; Conservative 0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1997
APPLICATION NUMBER: US 08/302,752
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PR FR92/03034
FILING DATE: 13-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR FR92/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAMM: PROCKET NUMBER: C93:31779
TELEPHONE: (626) 759-9900
TELEPHONE: (626) 777-8800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH. 3792 Base pairs
TWENEY. NUCLES ASIA
                                                                                                                                                                                                                           STREET: Thristie Parker & Hale, LLP STREET: 350 West Colorado Boulevard, Suite 500 CITY: Pasadena STATE: California COUNTRY: United States ZIP: 91105
3343 ACTAGTTAAAACTATTTCAGATAACGCAGGTAAA 3376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: YES : IMMEDIATE SOURCE: CLONE: pG+host4 US-08-992-334-1
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HYPOTHETICAL:
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2229 ATTGCACGAAATCCTGTAACAATAGAAAGCGTTAGGAACAAGATTAAGCGAAAATTGGGG 2288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           820 ATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTG 879
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Patent No. 5919678
GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000 ATCCATCATATGAATATTAAAGTTTTCAGCAACGGCTTAGATGATG 1045
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2409 Trgaacarraargarrirgararrgaccccrararacacrrgarg 2454
                                                                                                                                                                 Sequence 1, Application US/08302752
| Sequence 1, Application US/08302752
| Patent No. 6025190
| GENERAL INFORMATION:
| TITLE OF INVENTION: THERMOSENSIBLE PLASMID
| NUMBER OF SEQUENCES: 3
| COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC compatible
| COMPUTER: IBM PC compatible
| SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
| CURRENT APPLICATION NUMBER: US/08/302,752
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3671 ATTGCACGAAATCCTGTAACAATAGAAAGCGTTAGGAACAAGATTAAGCGAAAATTGGGG 3730
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Grues, Alexandra
APPLICANT: Grues, Alexandra
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES:
ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Passadena
STATE: California
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APPLICATION NUMBER: US/08/992,334 FILING DATE: 17-DEC-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.6;
Pred. No. 5.
                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PF 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR92/03034
FILING DATE: 13-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-752-2
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.2%;
Best Local Similarity 47.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                   LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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: United States
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3.2%; Score 35.6; DB 2; Length 5234;
Best Local Similarity 47.3%; Pred. No. 5.1;
Matches 107; Conservative 0; Mismatches 119; Indels 0
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APPLICATION NUMBER: US/08/302,752
                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THERMOSENSIBLE PLASMID
                                                                                                                                                                                                                 PAPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIPICATION: 435
FRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
FRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: FR FR92/03034
FILING DATE: 13-MAR-1993
ATPORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
FELECOMMUNICATION INFORMATION:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08302752
Patent No. 6025190
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THERMOSENSIBLE
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (626) 795-9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
California
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: both
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820 ATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTG 879
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                                                                                                                                                                                                                                                                                                      1000 ATCCATCATATAAATTTAAAGTTTTCAGCAACGGCTTAGATGATG 1045
                                                                                                                                                                                                                                                                                                                                                      5339 TIGAACATTAATGATTITGATATIGACCGCTATATAACACTIGAIG 5384
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                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-001C-650
; Sequence 650, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-134-001C-650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 TATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGAT 999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   880 TATCGTGCATCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5339 Tigaacariaargarrirgararigaccecrararacacrigarg 5384
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.2%; Score 35.6; DB 2; Length 6 Best Local Similarity 47.3%; Pred. No. 5.6; Matches 107; Conservative 0; Mismatches 119; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/302,752 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THERMOSENSIBLE PLASMID
                           NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-9900
TELEPHONE: (626) 795-9900
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR/93/00246
FILING DATE: 12-MAR-1993
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6025190
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THERMOSENSIBLE F
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/08302752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-302-752-3
                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic) US-08-992-334-3
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: ging
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US-08-302-752-3
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PRILING DATE: 1997-11-08
PRIOR PLING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 550
LENGTH: 1434
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Batent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2636
                                                                                                                                                     5219 AATAGTTCAGTFGCFCATGTFGAGATACTTGATTATATCAAAGGTTCATATGAATATTTG 5278
                                                                                                                                                                                                                                                                                                       5279 ACTCATGAATCAAAGGACGCTATTGCTAAGAATAAACATATATGGACAAAAAAGATATT 5338
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                                                                              880 TATCGTGCATCTGGTCAAGAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAA 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            612 TGATAAAATTTCTGTAGTTTATTCTACTTTCGGCTTTTGGTTTAATTTTATTCGCATTTAG 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               774 AGCAGATAGTCTACCTGCCACATTATTAGAAGTGGTTCCAATGACCATTGAAAGCATTCC
5159 ATTGCACGAAATCCTGTAACAATAGAAAGCGTTAGGAACAAGATTAAGCGAAAATTGGGG
                                                                                                                                                                                                                                940 TATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCACACGCTGAT
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987 TAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAGCAACGGCTTAGATGATGT 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 Gaaagaararaaararcrcarraaaaargrrrararrgagracargrrgaaraarrr 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                               927 IGCTAGTCCAGAATATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCACACT
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                     APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: DAGNOSIS OF LUNG CANCER
CURRENT PELICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 360
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CURRENT APPLICATION WHERE: US/09/736,457

CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                   Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                 77; Indels
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Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           2.8;
                                                                                                                                                                                                                                                                                                                                                 3.1%; Score 34.8;
51.3%; Pred. No. 2.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1408, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Tongtong
Bangur, Chaitanya S
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Best Local Similarity 51.3%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.33
Matches 81; Conservative
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Wang, Aijun
                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-736-457-1408
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SEQ ID NO 1408
LENGTH: 360
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APPLICANT:
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APPLICANT:
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Patent No. 6562958
GENERAL INFORMATION:
FALL INFORMATION:
FALLE OF INVENTION: BACOM et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BACMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3221
LENGTH: 4860
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Pred. No. 7.2;
0; Mismatches 45; Indels
                                                                                                              Score 35; DB 4; Length 927; Pred. No. 3.7; 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 CACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCATTTGCTG 313
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Patent No. 6504010
GENERAL INFORMATION:
                     ; TYPE: DNA; ORGANISM: Acinetobacter baumannii
US-09-328-352-2636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Acinetobacter baumannii
US-09-328-352-3221
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Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                                                 3.1%;
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Best Local Similarity 57.9%;
Matches 62; Conservative
                                                                                                            Query Match
Best Local Similarity 45.2
Matches 128; Conservative
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LENGTH: 927
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APPLICANT:
APPLICANT:
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APPLICANT:
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980 CACACCTTAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAGCAACGGCTTAG 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     920 GATTTCCTGCTAGTCCAGAATATCATGAAGCCACAGTTAAAATTCGTTAAGTTTATAAATC 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.1%; Score 34.8; DB 3; Length 1347; Best Local Similarity 48.5%; Pred. No. 4.9; Matches 96; Conservative 0; Mismatches 102; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1053;
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3.1%; Score 34.8; DB 4;
Best Local Similarity 52.0%; Pred. No. 4.4;
Matches 78; Conservative 0; Mismatches 72;
                   FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHOME: (791)893-5077
INFORMATION FOR SEQ ID NO: 3324:
SEQUENCE CHARACTERISTICS:
LENGTH: 1053 base pairs
TYPE: INGLES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1040 ATGATGTCCCAGCTCTCACTGAAGGTATAA 1069
    APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature;
CCATION: (B) LOCATION 1...1053;
SEQUENCE DESCRIPTION: SEQ ID NO: 3324:
US-09-107-532A-3324
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
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                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: S674
SEQ ID NOS: S674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     583 GTGAACTATCTAAAAATGAACTTCGTTTTGATGCTGGTATCGATTACAAAAAGATAAT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 CCTAAAGAAGGIGAAACAGTAGTTATTTCAGCAGCTTCAGGTGCAGTTGGTTCAGTTGTG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            559 ATCCAAGTTGCCAAACATATCAATGCTTATACTAAGATTGTAACTGTTGTTGCTTCTAAAAAG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 GGCChantidcGhagcrthaaggrtgcagagtcgrtggrafagcrggrggrgagaraaaa 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 CATGAAAAGCTTTTAAAGTCTTATGGTGCTGATGATGTCTTTGACTATCATGATGCAGGC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679 GTTATTGAGCAGATCAAATCGAAGTATCCAAACCTGCAACATGTTATTGACGCTGTGGGA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 TTCCCTGAAGCGTTAAAAGAAGCGGTGCCTAACGGTATAGATGTCTACTTCGAAAATGTA 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCAACATACTCCATCCATTATTGATTTGGGGTGGTGCTACAGCAGTGGGTCAACAACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34.8; DB 4; Length 1044; Pred. No. 4.4; 0; Mismatches 147; Indels 0
320 TATATTGTGACACATTGTGTTAAATAATAATAAAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      739 AGCGAAGATAGTATCCCCGAGGCCTATAAA 768
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US-09-107-532A-3324/c
; Sequence 3324, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                         ; Sequence 461, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.1%;
Best Local Similarity 45.6%;
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
                                                                                            RESULT 22
US-09-134-001C-461
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Sequence 131, Application US/09601198

Patent No. 6531583
GENERAL INFORMATION:
APPLICANT: Classell, Gail H.
APPLICANT: Class, Johnifer S.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UNCLETC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA; TITLE OF INVENTION: UNCLETC ACID PROBES
CURRENT APPLICANTON NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1998-01-30
1098 TTGATGCTGATCCTCTTGCCGTTGGCGCCTAACAGGCAAAAACTGTCATGATAAAGTGA 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               972 TATAAATCCACACCTTAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAGCAA 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916 TAATTATGATGAATTAAAATTAATGCGATTAATAATGATCATGAAGAATTAAGAGACCA 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        796 haaraacgraagragcarraacgcarcrggraarrragcaacarraaarggcrrrarrr 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    736 AAATGATTGTACACTACCAAATGATTTAACAACAGATAAAAGCAATAAAGTTTATGATAA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    732 TGTGGGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACAGCAGATAGTCTACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   976 igirrgrantarararananarcandrrracrancritancardargrarrrargr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          792 CACATTATTAGAAGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAATCAGAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 852 TAATGTTAAAATTGATATTACTTGTTGTATCGTGCATCTGGTCAAGAAATTCTATTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        912 IGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACAGTTAAATTCGTTAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
3.1%; Score 34.8; DB 4; Seet Local Similarity 43.3%; Pred. No. 4.9;
Matches 162; Conservative 0; Mismatches 212;
                                                                                                                                     1158 AGATACAATAGACTGTAT 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-131
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                                                                                   860 AAATTGATATTACTTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 131
LENGTH: 1374
                                                                                                                                                                                                                                               JS-09-601-198-131/c
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US-09-173-053-3
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                                                                                                    1098 frearderdarcerefrecearregeedecraacadecaaaaacrefreardaraagrea 1157
  1038 CCAGTGAAGTAGTCAATGAAGCATATTCAAGATTAGCATATTCTGCGTTATCCTCATTAC 1097
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                                                       800 TAGAAGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800 TAGAAGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTA 859
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                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09165922A

Patent No. 6348641

GENERAL INFORMATION:
APPLICANT: STILES, JOHN I.
MOISYADI, ISTEFO
NEUPANE, KABI R.
TITLE OF INVENTION: PURIFIED PROTEINS,
PRODUCING CAFFEINE FREE BEVERAGES

PRODUCING CAFFEINE FREE BEVERAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.1%; Score 34.8; DB 4; Length 1 Best Local Similarity 48.5%; Pred. No. 4.9; Matches 96; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: JONES, DAY, REAVIS & POGUE
STREET: NORTH POINT, 901 LAKESIDE AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: GRIFFITH, CALUIN P.
REGISTRATION NUMBER: 34,811
REFERENCE/DOCKET NUMBER: 265036600003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 556-7050
TELEPHONE: (216) 579-0212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v. 5.1
SOFTWARE: WORDERfect for Windows v.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/165,922A
FILING DATE: 02-Oct-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 53..1168
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                1158 AGATACAATAGACTGTAT 1175
                                                                                                                                                                 860 AAATTGATATTACTTTGT 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 44114
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: CLEVELAND
STATE: OHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                             US-09-165-922A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-165-922A-11
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14400 TGGGATGTTATTTGTACAGTAGTCTGACATTTAACTAATCAGATTTGTCATTTTTAGGTA 14459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14580 GGCAGATGCCTAAATGAAATCTCTACAGGACCTTGGAAGACCCTTGAACTTTTGCATTCA 14639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 TGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTGACTTGAAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCTGCTGCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 51259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 701 Fifth Avenue, Suite 6300 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                CURRAILS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRAIN APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6930
TELEPHONE: (206) 682-6931
INFORMATION POR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
STARNDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34.8; DB 3;
Pred. No. 21;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 209, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
Yu, Chang-En
OShima, Junko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZEP: 98104-7092.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                 COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.1%;
                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14640 GAĞTGAATTTTĞ 14651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 TTGCCAGTTTCG 432
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Best Local Similarity 49.2
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY:
US-08-781-891-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-618-166-209
  COUNTRY:
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                                                        APPLICANT: BARBOUK, Alan G.
APPLICANT: LUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING BORRELIA DNA TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING BORRELIA DNA FILE REFERENCE: 454312-2440.1
CURRENT APPLICATION NUMBER: US/09/173,053
PRIOR FILING DATE: 1998-10-15
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    983 ACCTTAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAGCAACGGCTTAGATG 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1043 ATGICCCAGCTCTCACTGAAG---GIATAAAAGAAGGTAAAAACAAAAATGTTAAGTATG 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      803 AAGTGGTTCCAATGACCATTGAAAGCATTCCTGAAGAAATCAGAAAAGATAATGTTAAAA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 TTAATATAAAAGGAGAATATATATGAAAAATATTTATTGGGAATAGGTCTAATATTAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 CCTTAATAGCATGTAAGCAAAATGTTAGCAGCCTTGACGAGAAAAAACAGCGTTTCAGTAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITGATATTACTTIGITGIATCGTGCATCTGGTCAAGAATTCTATTGGGTGCAACAAGAT 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITCCTGCTAGTCCAGAATATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAAATCCAC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 ATTIGCCIGGIGAAAIGAAGCIICTIGIAAGCAAAGAAAAAAAAGAGAGGCAAGIACG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTAGAACCAAACTTAATTAAAACCAAACTTAATTGAAGTTATTATCATTTTATTTTT 95
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Sequence 209, Application US/08781891

Seterat No. 6090620

GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Vu, Chang-En
APPLICANT: Oshima, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Cenrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.1%; Score 34.8; DB 4; Length 4 Best Local Similarity 47.0%; Pred. No. 7.6; Matches 142; Conservative 0; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) LOCATION: (1078)..(1085)
; OTHER INFORMATION: N stands for A or G or C or T US-09-173-053-3
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (6)..(29)
OTHER INFORMATION: N stands for A or G or C or
NAME/KEY: misc_feature
LOCATION: (1078)..(1085)
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Borrelia burgdorferi
                  LIANG, Xiaowu
CARNER, Kristin R.
BARBOUR, Alan G.
NORMAN. Jon A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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completed: January 10, 2004, 08:41:27
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Job time : 112 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14400 TGGGATGTTATTTGTACAGTAGTCTGACATTTAACTAATCAGATTTGTCATTTTTAGGTA 14459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 GGAGATACCGGTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 CACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCTGCATCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 TGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTGACTTGAAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 51259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Johnsondra K. Bhattacharjee
APPLICANT: Richard C. Garrad
APPLICANT: Paul L. Skatrud
APPLICANT: Paul L. Skatrud
TITLE OF INVENTION: Methods and Reagents for
TITLE OF INVENTION: Detecting Fungal Pathogens in a
TITLE OF INVENTION: Biological Sample
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDorrel'S
STRFF
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.1%; Score 34.8; DB 4; ilarity 49.2%; Pred. No. 21; Conservative 0; Mismatches 122;
                                                                                                                                                                               NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
                                                                                                 APPLICATION NUMBER: US/09/618,166
                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 209:
US-09-618-166-209
                                                                                                                      FILING DATE: 17-Jul-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word 7.0
                                                                                                                                                                                                                                                             TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                     (206) 682-6031
                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-60
INFORMATION FOR SEQ ID NO: 209:
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Best Local Similarity
Matches 124; Conserva
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973 AAAGATGTTAAAATTGAATTAGAAAAGCTTTAACTAAAATGGGGGTCAATATCCTAAA 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .093 ATTGGTATCCCTGATGATAATATTGCTAAATGGGATATGGCTGAAACTGCTAAAGGTGGT 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 ITAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 AAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AAAGCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.4; DB 2; Length 1 Pred. No. 7.1; 0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae
US/08/360,606B
                   December 21, 1994
                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Berghoff, Paul H.
REGISTRATION UNMBER: 30,231
REFERENCE/DOCKET NUMBER: 94,31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 913-0001
TELEFAX: (312) 913-0002
INPORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1153 CCATTCCAAGAAATTG 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 ACAGTTGTCAAACTTG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.1%;
                                                                                                                                                                                                                                                                                                                    1856 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.5
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                           linear
                     FILING DATE: DE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-360-606B-29
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81

10668 13 US-09-814-353-20029 Sequence 20029, A 10681 10 US-029-386-2543 Sequence 25433, A 11 US-0-29-386-2543 Sequence 25433, A 11 US-0-29-386-2543 Sequence 25433, A 11 US-10-252-157-159 Sequence 159, App	14 US-10-027-632-216679 Sequent US-09-070-927A-842 Sequent US-09-070-927A-842 Sequent US-10-070-923-4 Sequent US-09-800-065-3 Sequent US-09-98-117-79 Sequent US-09-98-117-79 Sequent US-09-98-117-79 Sequent US-09-98-2941-1408 Sequent US-09-98-98-626-1408 Sequent US-09-98-98-626-1408 Sequent US-09-98-98-98-98-98-98-98-98-98-98-98-98-98
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00 0 00000000 00 0 0 000 0 0 000 111119999999999	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  - nucleic search, using sw model  January 10, 2004, 07:53:26; Search time 448  (without alignmen 8627.273 Million 113	Pred. No. is the number of results predicted by chance to have a accore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.    Courty

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Sequence 14, Application US/10081644

Publication No. US20020192782A1

Publication No. US20020192782A1

Publication No. US20020192782A1

APPLICANT: Yamamoto, Hiroaki

APPLICANT: Xamamoto, Hiroaki

APPLICANT: Xamamoto, No. US20020192782A11hiro

TITLE OF INVENTION: NOVEL ENONE REDUCTASES, METHODS FOR

TITLE OF INVENTION: USING THE REDUCTASES

TITLE OF INVENTION: USING THE REDUCTASES

TITLE OF INVENTION: USING THE REDUCTASES

TITLE OF INVENTION: USING THE REDUCTASES

FILE REFERENCE: 06501-100001

CURRENT APPLICATION NUMBER: US/10/081,644

CURRENT PILING DATE: 2002-02-21

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PastSEQ for Windows Version 4.0

LENTH: 509
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Matches 501; Conservative 5; Mismatches 3;
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US-10-991-936-213
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                                                                                                                                                          GIGCATTIGCTGAATATGCCAGGCTTTATCCACCTTTGTTTTACAA-----GAGTAACT 355
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Sequence 3, Application US/10081644
; Publication No. US20020192782A1
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APPLICANT: Yamamoto, Hiroaki
APPLICANT: Yamamoto, No. US20020192782A11hiro
TITLE OF INVENTION: NOVEL ENDNE REDUCTASES, METHODS FOR
TITLE OF INVENTION: PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A
TITLE OF INVENTION: CARBON-CARBON DOUBLE BOND OF AN ALPHA, BETA-UNSATURATED KETONE
TITLE OF INVENTION: USING THE REDUCTASES
TITLE OF INVENTION: USING THE REDUCTASES
TITLE OF INVENTION: USING THE REDUCTASES
CURRENT FILING DATE: 2002-02-21
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 29
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 5
SEQ ID NO 5
LEASTHARE: PRICES FOR WINDOWS VERSION 4.0
SEQ ID NO 5
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ORGANISM: Saccharomyces cerevisiae
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; LOCATION: (1)...(1131)
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Publication No. US20020192782A1

Sequence 7, Application US/10081644

Publication No. US20020192782A1

GENERAL INFORMATION:
APPLICANT: Yamamoto, Hiroaki

APPLICANT: Yamamoto, No. US20020192782A1ihiro

TITLE OF INVENTION: NOVEL ENCUR ENDUCTASES, METHODS FOR TITLE OF INVENTION: PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A TITLE OF INVENTION: USING THE REDUCTASES

TITLE OF INVENTION: USING THE REDUCTASES

TITLE OF INVENTION: USING THE REDUCTASES

TITLE OF INVENTION: USING THE REDUCTASES

TITLE OF INVENTION: USING THE REDUCTASES

FILE REFERENCE: 06501-10000.

CURRENT FILING DATE: 2002-02-21

PRIOR PLILING DATE: 2001-02-23

NUMBER OF SEC ID NOS: 29

SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                           <u> CCTTACTTGGTGGACTGTGTCTCCAACACAAACTATTCAACAGGTGTACAAATGTGCC</u>
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                                                                 APPLICANT: Kimoto, No. US20020192782A11hiro
TITLE OF INVENTION: NOVEL BRONK REDUCTASES, METHODS FOR
TITLE OF INVENTION: RODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A
TITLE OF INVENTION: CARBON-CARBON DOUBLE BOND OF AN ALPHA, BETA-UNSATURATED KETONE
TITLE OF INVENTION: USING THE REDUCTASES
FILE REPERBENCE: 06501-100001
CURRENT APPLICATION NUMBER: US/10/081,644
CURRENT PILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: JP 2001-49363
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58.8%; Pred. No. 4.9e-84;
iive 0; Mismatches 452
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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                                    Hiroaki
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Matches 658; Conserv
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US-10-081-644-3
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3.50 inch, 1.4Mb

STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4N
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:

ATTORNEY/AGENT INFORMATION:

FILING DATE:

CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:

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973 ATAAATCCACACCTTAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAGCAAC 1032
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                                                                                                                      250 handschicaricaccearchicchaagerricchrocaardsrichtriccidaarai 309
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                                                                                TTCGGTTTTTGTTCACGGTGCTTCCCCAAACAGATCCTAAAAATGGTGCATTTGCTGAATAT
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US-10-029-386-25419/C
; Sequence 25419, Application US/10029386
; Sequence 25419, Application US/10029386
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Harzel, David R.
; APPLICANT: Harzel, David R.
; TITLE OP INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15838 TGATCGTAGACCTAATGACGAAGCAATCACTATTTATCGTAAAGTTGTTGATTTCTTAAA 15779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15958 ACCTGTTTTCATTGCGCATTGTAATGGCGATTATGATGTTCCCGTTGAGGAAAGCGAACA 15899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15898 TATCATGAATCATGTTCCACATTCAACATTTGAACGCGTGAATAAAAACGAGCATGATTT 15839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   744 AGATAGTATCCCCGAGGCCTATAAAGTCACAGCAGATAGTCTACCTGCCACATTATTAGA 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 AGTIGCCAAACATATCAAIGCTTATACTAAGATIGTAACTGTIGCTTCTAAAAAGCAIGA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           624 AAAGCTTTTAAAGTCTTATGGTGCTGATGATGTCTTTGACTATCATGATGCAGGCGTTAT 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 ACATACTCATCCATTATTGATTTGGGGTGGTGCTACAGCAGTGGGTCAACAACTAATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       684 TGAGCAGATCAAATCGAAGTATCCAAACCTGCAACATGTTATTGACGCTGTGGGAAGCGA
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                                                                                                                                                                                                                                                                                                                                                                                          Score 45.4; DB 8; Length 23439;
Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 196;
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                        TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            45.48;
                                                                                                                                                                                                                                LENGTH: 23439 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-781-986A-38
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   STRANDEDNESS
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RESULT 6
US-08-781-986A-38/c
US-08-781-986A-38/c
; Sequence 38, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

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Sequence 2, Application US/10312841

Publication No. US20030186277A1

GENERAL INFORMATION:

TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC

TILE REFRENCE: E01/1208/WO

CURRENT APPLICATION NUMBER: US/10/312,841

CURRENT FILING DATE: 2002-12-30

NUMBER OF SEQ ID NOS: 2
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APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
3131933 TTAAAAACAATTACCGTATAATATTTTTTTTTTTTTTATATAAACACATAATATATATC 3131874
                                                                                                                                                                                                                                                                       3131754
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                                            CAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACAGTTAAATTCGTTAAGTTTATAA
                                                                                    977 ATCCACACCTTAACAACGGTGATATCCATCATATGAATATTAAAGTTTTCAGCAACGGCT
                                                                                                                                                                             896 AAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694104 ААААААТААААТАААТАААДАДАТАТТАСАСААААССАААТАТААТТТАААСТТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       956 TTAAATTTCGTTAAGTTTATAAATCCACACTTAACAACGGTGATATCCATCATATGAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 693924 AAAATAAAATAACATAAAAATTATCACAAATTTA 693890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40.6; DB 13;
Pred. No. 3.8e+02;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1076 GTAAAAACAAAATGTTAAGTATGTTGCCAGGTTA 1110
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; Sequence 20174, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  3131693 AACTTACCCTTTTATAA 3131677
                                                                                                                                                                                                                                                                                                                      ATGTTGCCAGGTTATAA 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 49.3%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (379615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3673778
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Publication No. US20030186277A1
GENERAL INFORMATION:
FAPELICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: B01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 GATGTAAGTGGTGTCAATATTGTTGATGTTGGTGGTTGATGGTGGTGGTATTGATGTT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 TGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTGACTTGAAGGTT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 GCTGATGCTGATGTTGGTGTGTCAATATTGTTGATGTTGGTGATGTTGATGTTCTTGAT 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GITCCAACCACTCAAAAAGCCGTCATCATTGAAGGTGACAAAAGCTGTTGTTAAAACAGAT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 13; Length 3673778; Pred. No. 3.2e+02; 0; Mismatches 135; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                              Query Match
3.7%; Score 41; DB 13; Length 572;
Best Local Similarity 45.7%; Pred. No. 2.1;
Matches 143; Conservative 0; Mismatches 170; Indels
                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AL079336.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.62
OTHER INFORMATION: NT HIT: AF128626.1, EVALUE 1.40e-01
US-10-029-286-28419
           FILE REFERENCE: AECMICA-x-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SEQ ID NO 25419
LENGTH: 572
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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Best Local Similarity 47.5%;
Matches 122; Conservative C
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                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (3294164)
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205 TCCTGCTGATGTTTTGATGTTATGATGTGTGATGCTGCTGACGTGATGATGTGA 146
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265 TGCTGATGGTGATGGTGGTGGTGATTACGATGGTGATGCTGCTGCTGCTGCTGGTGGTGA 206
                                                      216 TGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 CATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACA 204
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                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/1007584;
Publication No. US20030073610A1
GENERAL INFORMATION:
APPLICANT: LINDQUIST, SUSAN
APPLICANT: LINDQUIST, SUSAN
APPLICANT: OUTER, SYLVIA
APPLICANT: OUTER, SYLVIA
APPLICANT: OUTER, SYLVIA
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APPLICANT: OUTER, SYLVIA
APPLICANT: OUTER, SYLVIA
CURRENT APPLICATION NUMBER: US/10/077,584
CURRENT APPLICATION NUMBER: 60/269,157
PRIOR PILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 GCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGTCAAACTTGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGT
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45.7%; Pred. No. 6.2;
iive 0; Mismatches 165;
                                                                                                                                                                                                                              145 reargargargarantaricardardicin 117
                                                                                                                                                                       276 TGCTTCCCAAACAGATCCTAAAAATGGTG 304
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Publication No. US20030235833A1
GENERAL INPORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.7
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h NAME/KEY: CDS

LOCATION: (1)..(513)

US-10-077-584-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 AGCCTTGGTGAAGGTTGAGGCTGTTGCTGAACCCAACTGATTGGAAGCATATTGCTTA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 reccarderarderdardardardarderacerecrecidardererreardecearde 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 TGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTAC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N BONE MARROW, SIGNAL = 1.3
N LUNG, SIGNAL = 1.2
N HELA, SIGNAL = 1
N BRAIN, SIGNAL = 1.4
N HBL100, SIGNAL = 1.1
N PLACENTA, SIGNAL = 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40.2; DB 9; Length 4 Pred. No. 3; 0; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN ADULT LIVER, SIGNAL = 1.6
IN HEART, SIGNAL = 1.5
IN BT474, SIGNAL = 1.5
IN FETAL LIVER, SIGNAL = 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20174
LENGTH: 439
            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
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OTHER INFORMATION: EXPRESSED IN LUN
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OTHER INFORMATION: EXPRESSED IN ADI
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US-09-864-761-20174
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Best Local Similarity 46.8%;
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity
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uB-10-

"TITLE OF INVENTION: GUANGSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS;
FILE REFERENCE: 084318/166

CURRENT PELLING DATE: 2002-11-13

PRIOR PELLING DATE: 2002-11-13

PRIOR PELLING DATE: 2001-12-18

PRIOR PELLING DATE: 2001-12-18

PRIOR PELLING DATE: 2001-12-18

PRIOR PELLING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1825

LENGTH: 116R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1620, Application US/09878574

Fatent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT APPLICATION NUMBER: US/09/878,574

FILE REPLIANG DATE: 2001-12-21

FRIOR FILING DATE: 1990-06-14

NUMBER OF SEQ ID NOS: 15775

LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 AGCCTTGGTGAAGGTTGAAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 TGATGGTGGTGATGATGGTGGTGATGGTGATGACAGTGATGGTGGTGGTGGTGAGGATGA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 TGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 TGATGGTGATGATGATGCTGGTGATGATGATGGTGATAATGATGGTGGTGATGGTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 TGGTGGTGATGATGGTGGTGAGGATGATGGTGACGATGGTGGTGATGATGATGGTGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 TGCTTCCCAAACAGATCCTAAAATGGTGCATTTGCTGAATATGCCAGGGTTTAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 39; DB 12; Length 11
45.8%; Pred. No. 11;
ive 0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
) OGGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-035-Q1-B1-E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 45.8 Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: CDS
) LOCATION: (201)..(968)
US-10-292-798-1825
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1) .. (1168)
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DB 10; Length 392;

Score 38.8;

3.5%;

Query Match

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029;386
CURRENT FILING DATE: 2001-112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20619
LENGTH: 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 GCCTTGGTGAAGGTTGAGGCTGTTGCTGGTAACCCCAACTGATTGGAAGCATATTGCTTAT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 GATGGTGGTGATGATGGTGATGGTGATGATGACAGTGATGATGATGGTGGTGAGGATGAT
                                                                                                      529 GGTGGTGCTACAGCAGTGGGTCAACAACTAATCCAAGTTGCCAAACATATCAATGCTTAT
                                                                                                                                                                         103 GGAGGTGCTGGTGGAGTTGGAACCCATGTTATTCAGCTTGCCAAGCATGTTTATGGAGCA
                                                                                                                                                                                                                                                                                                            163 rccaaggragcagcracrgcragcacraggaacraggaacraraaggaarrraggagcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 GAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 GGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTTGGTTTTGTTCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 GGTGGTGATGGTGGTGGTGAGGATGATGGTGACGATGGTGGTGATGATGATGATGATGATGAT
                                                                                                                                                                                                                                            589 ACTAAGATIGIAACTGTIGCTICTAAAAAGCAIGAAAAGCITITIAAAGICTITAIGGIGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AAGATTGGTCCAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACTT
                                   Gaps
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
                                   Indels
                                   62;
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ilarity 45.6%; Pred. No. 12;
Conservative 0; Mismatches 160;
   Pred. No. 6.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20619, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-017-161-2179
; Sequence 2179, Application US/10017161
                                                                                                                                                                                                                                                                                                                                                                                                                                               223 GACTGGCCTATTGATTAT 240
ilarity 55.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                  649 GATGATGTCTTTGACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Matches 134; Conserv
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PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SEQ ID NO 20029
LENGTH: 10668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1077 TAAAAACAAAATGTTAAGT 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5367 TAAGAACATAAATTAAAAT 6348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09790988
Patent No. US20020127687A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.6%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 640681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 GGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGGT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 GATGGTGATGATGATGCTGCTGATGATGATGGTGATAATGATGGTGATGGTGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 GAAGGIGACAAAGCIGTIGTTAAAACAGAIGTCTCAGTTCCAGAATTAAAGGAGGGIACA 96
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Sequence 20029, Application No. US20030165831A1

Sebblication No. US20030165831A1

APPLICANT: Lee, John

APPLICANT: Lillie, James

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: UNBER: US/09/814,353

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT APPLICATION NUMBER: US 60/207,124

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PLING DATE: 2000-05-25

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: US 60/211,940

PRIOR PLING DATE: US 60/216,820

PRIOR PLING DATE: US 60/216,820

PRIOR PLING DATE: US 60/216,820
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                                                                                     APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT APPLICATION NUMBER: JP 2001/246789
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PRENTIN Ver. 2.1
SEQ ID NO 2179
                     GENERAL INFORMATION:
APPLICANT: SUWA, WAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
    Publication No. US20030143668A1
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (201)..(968)
US-10-017-161-2179
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: source
LOCATION: (1)..(1168)
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547422 AATTAGTTATTGAGATGGAAACTAACGGAACTATTGATCCAGAAGAAGAAGTTTCGACGAG
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                                                                                                                                                                                                                                                                                                                                                                                                  5607 AGTCAGCAGAGCAGCCACTGTTTGTCAAAAATCTACTGTGTCCTTTAGCACTTAAAGCCA 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5547 GCTCTATCTÁTAAAGCAAGAAAACAGTGACACACÁCTGCÁCATAATTGTTAAGAAAGAAA 6488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        897 AGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 AACATGTTATTGACGCTGTGGGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACAG
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APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790, 988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR APPLICATION NUMBER: JP2000-10716
SOFTWARE: PATENTING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
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                                                                                                                                                                                       Length 10668;
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18.6%; Pred. No. 1e+03;
tve 0; Mismatches 109;
                                                                                                                                                                                Query Match
3.4%; Score 37.6; DB 13;
Best Local Similarity 46.5%; Pred. No. 97;
Matches 121; Conservative 0; Mismatches 139;
NAME/KEY: misc_feature; LOCATION: 10568; LOCATION: 10556, 10593, 10616, 10641, 10668; US-09-814-353-20029
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 CAGAAGGTTCAATTCTAGGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 CTAGTACTGACTTGAAGGTTGGAGATACCGGTTTTCGTTTTGTTCACGGTGCTTCCCAAA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 835;
                                                                                                                                                                                                                                        INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
INFORMATION: SAFESSED IN LUNG, SIGNAL = 1.3
INFORMATION: SMISSPROT HIT: 029522, EVALUE 1.80e+00
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NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 22786
LENGTH: 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.2; DB 12;
Pred. No. 34;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.4%; Score 37.4; DB 13; Best Local Similarity 48.0%; Pred. No. 24; Matches 107; Conservative 0; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42193, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                      MAP TO AC006549.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.3%;
Best Local Similarity 48.6%;
Matches 102; Conservative
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                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: MOTHER INFORMATION: B OTHER INFORMATION: B OTHER INFORMATION: B OTHER INFORMATION: B OTHER INFORMATION: B OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         US-10-029-386-22786
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386 CURRENT FILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 34288 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-029-386-22786/c

Sequence 22786, Application US/10029386

Sequence 22786, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                      547362 CAGCTACTATTTTAGCAGAACAACTAGAAGCATTTGTTGATTTAAGAGATATTCGTGAAC 547303
                                                                                                                     547302 CTGAATTCAAAGAAGAAAAACCTGAATTTGAACCTATTTTGTTACGTCCAGTAGATGTT 547243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 TGGACCAAATGCTAGTACTGACTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 TGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTAC 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: MAP TO ALL132232.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.16
OTHER INFORMATION: NT HIT: U63807.1, EVALUE 8.50e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
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3.4%; Score 37.4; DB 13;
al Similarity 45.4%; Pred. No. 19;
134; Conservative 0; Mismatches 161;
                                                                        836 AAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTT
                                                                                                                                                                                                                 547242 rágaacrracagrrcgrrcrgcraarrgrcrr 547211
                                                                                                                                                                       896 AAGAAATTCTATTGGGTGCAACAAGATTTCCT 927
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; Sequence 25433, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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SEQ ID NO 25433
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Matches
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LENGTH: 8772
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                                                 1020 AGTITICAGCAACGGCTTAGATGATGTCCCAGCTCTCACTGAAGGTATAAAAGAAGGTAA 1079
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                                                                                 285 AGATGGTGAGCTTTGGTCTAATTATGTTAAAGGAATGATTGTCATGCTTAAAGGAGCAGG 344
225 CTCAGAAAATTTTCCTAAATTAGGCGTCATTGAATTTGATTTAGATGAAGTTGAAAAGAA 284
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Publication No. US2003009974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: W, Yongyao
APPLICANT: W, Yongyao
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REPERENCE: MRI-04)
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: G/306,220
FRIOR APPLICATION NUMBER: 60/306,220
FRIOR APPLICATION NUMBER: 60/306,220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030190640A1 903479.3
                                                                                                                                                                                                                                                                                                                               Sequence 159, Application US/10252157
Sequence 159, Application US/10252157
Publication No. US20030190640A1
GENERAL INFORMATION:
FAPPLICANT: Fearson, Cecelia I.
FITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
FILE REPERENCE: PA-0027-1 US
CURRENT APPLICATION NUMBER: US/10/252,157
CURRENT APPLICATION NUMBER: 60/295,048
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR PALLNG DATE: 2001-05-31
SPRIOR PLING DATE: 2001-05-31
SEQ ID NOS: 501
SEQ ID NOS: 501
SEQ ID NO 159
LENGTH: 7536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 3017-3175, 5473, 5489, 5500, 5504, 6570; OTHER INFORMATION: a, t, c, g, or other US-10-252-157-159
                                                                                                                                                      1080 AAACAAAATGTTAAGTATGTTGCCAGGTT 1109
                                                                                                                                                                                                          345 ATATGAAATTGACAAAGGTTTTGAATTGTT 374
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ORGANISM: Homo sapiens
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US-10-198-846-14020/c
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NAME/KEY: unsure
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                                                                                                                                                                                                                                    Length 7772;
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                                                                                                                                                                                                                              Query Match 3.3%; Score 37.2; DB 15; Best Local Similarity 51.9%; Pred. No. 1e+02; Matches 84; Conservative 0; Mismatches 78;
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Pred. No. 1.2e+02;
0; Mismatches 45;
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; Sequence 3, Application US/09788711A
; Sequence 3, Application US/09788711A
; Ratent No. US20020058328A1
; GENERAL INFORMATION:
; APPLICANT: Tania Tamein Testa
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30225
; CURRENT APPLICATION NUMBER: US/09/788,711A
; CURRENT FILING DATE: 2000-02-19
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NOS: 4
; SEQ ID NO 3.
; INMUTH. OF SECOND WINDOWS VERSION 3.0
; SEQ ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTHER TARGET ON US/09788711A
FACERT NO. US20020058328A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30225
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US/09/788,711A
CURRENT FILING DATE: 2001-02-20
FRIOR APPLICATION NUMBER: 004196.2
FRIOR PILING DATE: 2000-02-19
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FREESEQ for Windows Version 3.0
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 14020
LENGTH: 7772
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Best Local Similarity 58.7%;
Matches 64; Conservative
                                                                                                                                          CRGANISM: Homo sapiens US-10-198-846-14020
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US-09-788-711A-3
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CDS (12927) .. (13090)
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ACCATION: (11163)..(11385)
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(15856)..(16039)
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(17972)..(18181)
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COCATION: (19545)..(19712)
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(11929)..(12017)
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(14989)..(15130)
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(15312)..(15432)
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(16226)..(16327)
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(17669)..(17763)
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(18702)..(18885)
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LOCATION: (19231)..(19411)
                                                                                                                                                                                                                                                                                                                                                                                                               (11634)..(11749
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(19001)..(19129)
                                                                                                                                                                                                                                                                                  (8553)..(9200)
                                                                                                                                                                                                                 (201)..(3510)
                                                              ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
                                                                                                                                                     LOCATION: (1)..(24370)
                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                              NAME/KEY: CDS
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  SEC ID NO 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LifeSpan Biosciences
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 1920-44
CURRENT APPLICATION NUMBER: 06/227,144
PRIOR PRILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin Version 3.1
SEQ ID NO 523
LENGTH: 10531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 931, Application US/10292798
; Sequence 931, Application US/10292798
; Publication No. US200325833A1
; Beblicant: SUMA, MAXIXO
; APPLICANT: SUMA, MAXIXO
; APPLICANT: ASAI, KIYSANA, YUTAKA
; APPLICANT: ABUATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                             11 CAACCACTCAAAAAGCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCT 70
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                                                                                                                                                                                                                                                                             71 CAGTICCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGT 119
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                                                                                                      Score 37; DB 9; Length 8871; Pred. No. 1.2e+02; 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          US-10-225-567A-523/c
; Sequence 523, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
                                                                                                        Query Match 3.3%;
Best Local Similarity 58.7%;
Matches 64; Conservative
                    TYPE: DNA
CORGANISM: HOMO SAPIENS
US-09-788-711A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-523
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LENGTH: 8871
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                   169231 ATTCATTTTAAGAAATATACTAAAATGTAATAACTTGTACTTTTCCCATCCCACTTTGC 169172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169111 GTGTAGGTTTTCTTTTTTTTTTTAATACAGGATTACCTACAGAGGAACTAAACAT 169052
                                                                                                                                                                                                                                                                                                                                                                                                                   169171 TTTTCTAAGCAGTATTTATGTATTTCAACTTTTTTTACAGTTTAAATACAATATACTTAG 169112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      949 GCCACAGTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCAT 1008
                                                                                                                                                                                                                                                             829 ATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTGTTATATCGTGCA 888
                                                                                                                                                                                                                                                                                                                                                                   889 TCTGGTCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAA
                                                                                                                                                                                                             ô
; TYPE: DNA; ORGANISM: Homo sapiens; PERJURE: PERJURE: OTHER INFORMATION: Genbank Accession No. US20020142981A1 X87344 US-09-880-107-3814
                                                                                                                                                     Length 198285;
                                                                                                                                                     Score 37; DB 10; Length 19
Pred. No. 7.7e+02;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR PELLING DATE: 2001-09-23
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-36
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-09-03
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
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R APELICATION NUMBER: PCT/USO1/00669
R FILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
R RILING DATE: 2001-01-30
R APELICATION NUMBER: PCT/USO1/00668
R RILING DATE: 2001-01-30
R PILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
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R FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1009 ATGAATATTAAAGTTTT 1025
                                                                                                                                                     Query Match
Best Local Similarity 49.2%;
Matches 97; Conservative
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US-09-864-761-3403/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CAACCACTCAAAAAGCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACAGATGTCT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Sequence 3814, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR PLING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/231,054

PRIOR PLING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3814

LENGTH: 198285
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3.3%; Score 37; DB 12; Length 24370;
Best Local Similarity 58.7%; Pred. No. 2.3e+02;
Matches 64; Conservative 0; Mismatches 45; Indels 0
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; LOCATION: (24143)..(24170)
US-10-292-798-931
                                                  CDS
(20054)..(20254)
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(20547)..(20721)
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(22399)..(22526)
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(22761)..(22849)
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(22954)..(23148)
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(23287)..(23457)
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LOCATION: (23557)..(23791)
LOCATION: (19815)..(19941)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    894 TCAAGAAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGAAGCCAC 953
                                                                                                                                                                           1916 gaaactaarrereerreeraareareraeraerrecriterreceacrearecrecer
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                                                                                                          594 GATTGTAACTGTTGCTTCTAAAAGCATGAAAAGCTTTTAAAGTCTTATGGTGCTGATGA
                                                                                                                                                                                                                                                       654 TGTCTTTGACTATCATGATGCAGGCGTTATTGAGCAGATCAAATCGAAGTATCCAAACCT
                                      Gaps
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APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Kamamoco, Robert T.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROKATYOUS
TITLE OF INVENTION: PECKATYOUS
TITLE OF INVENTION WIMBER: 00/101,078
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/101,078
PRIOR APPLICATION NUMBER: 60/206,848
FRIOR PILING DATE: 2000-05-23
FRIOR PILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
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FRIOR PILING DATE: 2000-11-27
FRIOR PILING DATE: 2001-12-22
FRIOR PILING DATE: 2001-12-22
FRIOR PILING DATE: 2001-12-22
FRIOR PILING DATE: 2001-12-12
FRIOR PILING DATE: 2001-12-16
FRIOR FILING DATE: 2001-12-16
FRIOR PILING DATE: 2001-12-16
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FRIOR FILING DATE: 2001-12-17
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Pred. No. 76;
0; Mismatches 217; Indels
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Patent No. US20020061569A1
GENERAL INFORMATION:
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ORGANISM: Enterococcus faecalis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(969)
   Best Local Similarity 43.5%;
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert
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Sequence 243, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: SAWE, AND METHODS OF USE

TITLE OF INVENTION: SAWE, AND METHODS OF USE

TITLE OF INVENTION: SAWE, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT PILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AGGTTGAGGCTGTTGCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 Aregricarecriscriscriscriscriscristricarecristriscristricaristricaris 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 CTAGTACTGACTTGAAGGTTGGAGATACCGGTTTTCGGTTTTGTTCACGGTGCTTCCCAAA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 AGGGTAATAATGGTAATGATGGTGATGGCGATGATGATGATAATAACGATGATGCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 grádicardargicargcraciócrorriccacrdargar 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLIANG DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 3403
LENGTH: 441
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PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

LENGTH: 3150
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.8%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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US-09-938-842A-243/c
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Length 3150;

Score 36.8; DB 10;

3.3%;

Query Match

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US-09-815-242-6606
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Query Match 3.3%; Score 36.6; DB 9; Length 969; Best Local Similarity 58.9%; Pred. No. 43; Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps

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Search completed: January 10, 2004, 10:03:48 Job time : 477 secs

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                                                          complement (<185. .>1007)
/note="similar to Saccharomyces cerevisiae ORF YNL134c similarity to C.carbonum toxD gene ]
i putative frameshift(8)"
                                                                                                                                                                                                                                                                      cerevisiae ORF YCR102c
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similar to Saccharomyces cerevisiae ORF YLR460c
similarity to C.carbonum toxD protein ]"
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Pred. No. 2.1e-62;
2; Mismatches 314;
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:
2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:
3 ruis Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:
Regref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bacomyces baccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveromyces marxianns var. marxianns, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of the other extremity of this insert.
                           BX414650 BX414650
BZ869915 CH240 275
BZ86915 CH240 275
BZ065414 Drosophil
C92181 C92181 Dict
BX384819 BX384819
A1374249 T6453 WVA
BZ955772 CH240 96B
BJ371293 BJ371293
BQ914346 QHB.0B04,
BZ927574 CH240 77N
BZ913257 CH240 77N
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BZ913257 CH240 53F
BZ914511 CH240 56G
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Souciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrans, P., Lepingle, A., Liorette, B.,
Malpertuy, A., Neuvejlise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F.,
Galilardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 9.
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/strain="CBS 3082"
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E (bases 1 to 881)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., Genorin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis var. belaryomyces hansenii, var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida troplicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Bolotin-Fukuhara, M., Bon, B., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, C., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FEBS Lett. 487 (1), 3-12 (2000)
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PEBS Lett. 487 (1), 47-51 (2000)
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1; Mismatches 263; Indels
1072 GAAGGTAAAAACAAAATGTTAAGTATGTTGCCAGGTTATAA 1113
                                           226 GCAGGTAAGAATTCGGGTGTCAAATTTGTTGCAGCTTTGAAA 185
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/mol_type="genomic DNA"
/strain="CBS 4311"
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/note="similar to Saccharomyces cer
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/clone="ATOAA012G10"
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Best Local Similarity 56.9
Matches 350; Conservative
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Direct Submission

Direct Submission

Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
Seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS la part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveromyces thermocletans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
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Eukarycta; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (Dases I to 1072)
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Librente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P., and Weissenbach, J.
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   358 ACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCT
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                                                                                                                                                                                                                                                                              Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequencingenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to Saccharomyces cerevisiae ORF YLR460c similarity to C.carbonum toxD protein ]" /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerevisiae ORF YNL134c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 AC---CGTCCCATTGCCTCAACTGGACGACGAATACGTCTTGATCAAGACCAAAGCCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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۲.
the hemiascomycetous yeasts:
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Pred. No. 3.3e-34;
0; Mismatches 328; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4133. .>877
/note="similar to Saccharomyces cerevi
similarity to C.carbonum toxD gene ];
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Saccharomyces servazzii"
|mol_type="genomic DNA"
/strain="CBS 4311"
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231 c 205 g 209
                                 Saccharomyces servazzii
FEBS Lett. 487 (1), 47-51 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:27293"
/clone="AT0AA012G10"
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/note="end : T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGTGAAAGTGGATTCGAATACTGTCTTCAAGTTCCCACAAAAATTAACTTATTCTAAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 GCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATCTGCTGCATCATTGCCAGTT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 TCGTTGACAACTGCTGGTGTTAGTTTGTGTCATCACTTGGGCTCAAAATGGAATGGCAC 489
                                                                                                                                                                                                                                                                                                        A2931755
474.dhz89£64.sl Saccharomyces unisporus NRRL Y-1556 Saccharomyces unisporus Genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces unisporus
Saccharomyces unisporus
Sackaryotes unisporus
Eukaryotes, Pungi, Ascomycota, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements comparative DNA sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 AAGAATAATATCGAGGCAGGTAAATTTGACACTTGGGAAGCTTGTGCTAGTTTCCCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 GGTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCATTTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRATTTGARACCECTTTAGCTGCTGTTTTCTACGAATTAAAATTGAAACTTGAATGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="MRRL Y-1556 (CBS 398)"
/db xref="texcn:27294"
/clone="474.dhz89f04.81"
/clone="474.dhz89f04.81"
/clone lib="Saccharomyces unisporus NRRL Y-1556"
/note="Random genomic sequence"
97 c 79 g 158 t
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                                                                                                                                        13.2%; Score 146.6; DB 28; Length
58.2%; Pred. No. 1.18-25;
ive 0; Mismatches 194; Indels
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                                                                                                  630 TITAAAGTCTTAIGGIGCIGAIGAIGICTTIGACTAICAIGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Saccharomyces unisporus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8212, 4566 Scott Ave., St. Louis,
Tel: 314 362 2735
Fax: 314 362 7855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
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GSS.
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Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451
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/mol type="genomic DNA"
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/clone="XAT0AA001D07"
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces ervazzii, Zygosaccharomyces rouxii, Saccharomyces Stuyveromyces thurmotiolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                                                            GATGCAGGCGTTATTGAGCAGATCAAATCGAAGTATCCAAACCTGCAACATGTTATTGA 728
                                     rcaaagaaacarcaaaagarcrraaaarccrrriggrgcagargaagrgrrcgarrarcar 63
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Lepingle, A., Ilorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekfano, Toffano, Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
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/note="similar to Saccharomyces cerevisiae ORF YNL134c
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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/clone="XAT0AA002A04"
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434 bp DNA linear GSS 01-APR-2001 474.dhz89f03.s1 Saccharomyces unisporus NRRL Y-1556 Saccharomyces unisporus genomic clone 474.dhz89f03.s1, genomic survey sequence.
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Saccharomyces unisporus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
cerevisiae ORF YCR102c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 GAGATACCGGTTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                  DB 29; Length 1118;
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                                                 similarity to C.carbonum toxD gene
2 putative frameshift(s)"
/evidence=not_experimental
a 217 c 202 g 328 t 5
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                                                                                                                                                                                                                                                                                                                                                                  Score 137.2; DB 29;
Pred. No. 3.3e-23;
1; Mismatches 294;
     /note="similar to Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ931754.1 GI:13502665 GSS.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.1%;
Matches 379; Conservative
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/clone lib="min-3xHA/lacz Insertion Library"
/note="Vector: pHSS6-Sal; A yeast ganomic DNA library
(lacking mitochondrial DNA) was prepared in pHSS6-Sal;
genomic DNA was size-fractionated (DNA of roughly 2-3 kb
in length) prior to cloning. This library was
mubsequently mutagenized with a min-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-1999
Umanaky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 regarrecagaaaceargaaagecerrerearreaaaargecaaggererageaacag 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 GACATTCCAATTCCTGAATTAGAAGAACGATTTGTTCTAATTAAGACTGTCGCCGTTGCC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 GGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAATTCTA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 GGTAACCCTACCGATTGGAACATATTGATTTCAAGATTGGTCCTCAAGGTGCCTTCTTA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTG---ACTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 GGCTGTGATGCAGCCGGCCAAATCGTAAAGTTGGGCCCAAATGTTGATGCTGCACGCTTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GCCATTGGTGATTACATTTATGGGGTTATTCACGGTGCTTCAGTGAGGTTCCCCTCAAAC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ873738 SAChacz Insertion Library, strain AB972 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TCAGTTCCAACCACTCAAAAGCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Bukaryota, Pungli, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 GATGTCTCAGTTCCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGCT
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                                                                                                                                                 Dev. Biology
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Pred. No. 1.1e-20;
0; Mismatches 109; Indels
                                                                                                                      Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Bi
Yale University
Yob Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db xref="taxon; 4932"
/lab_host="E. coli"
                                                                                                                                                                                                                                                                  Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seg primer: GGCCTTCTTTCTTTGGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                   Seg primer: GGCCTTCTTTCT
Class: transposon-tagged
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AQ873738.1 GI:6285982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%;
al Similarity 64.7%;
205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                       Unpublished
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Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,
desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R.,
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  Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M. Surveying Saccharomyces genomes to identify functional elements b comparative DNA sequence analysis
Unpublished
Contact: Johnston M
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="NRRL Y-1556 (CBS 398)"
/db xref="texon:72294"
/clone="44.4dx3029f3.81"
/clone="144.dhz89f03.81"
/clone=lib="Saccharomyees unisporus NRRL Y-1556"
/note="Random genomic sequence"
76 c 88 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 132.6; DB 28; Length 434;
Pred. No. 3.4e-22;
0; Mismatches 159; Indels 6;
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Washington University Medical School
Washington University Medical School
Washington University Medical School
Washington University Medical School
Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mj@enetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
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al Similarity 59.7%;
244; Conservative (
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genomic 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"

fatrain="AB972 - trpl r(0) ($288C background)"

/db xref="taxon:4932"

/lab host="E. coli"

/lab host="E. coli"

/clone lib="mTn-3xHA/lacZ Insertion Library, strain AB972"

/note="Yector: pHSS6-Sal; genomic DNA library was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance.
Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Unpublished
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strain AB972 Saccharomyces
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                                                                                                                                                            and Dev. Biology
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Pred. No. 2e-20;
0; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                organism="Saccharomyces cerevisiae"
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Saccharomyces cerevisiae
                                                                                                                                     Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell.
Yale University
P.O. Box 208103, New Haven, CT 06520
Fax: 203 432 9949
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                                                                                                                                                                                                                                                 Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seg primer: GGCCTTCTTTGGAAGTAC
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Location/Qualifiers
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Matches 204; Conservative
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(DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lacz minitransposon containing lacz, URA3, and tet resistance.
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/#strain="ABB972 - trpl r(0) (S288C background)"
// strain="ABB972 - trpl r(0) (S288C background)"
// lab_host="E.coli"
// lab_host="E.coli"
// clone lib="mIn-3xHA/lacz Insertion Library, strain AB972"
// clone lib="mIn-3xHA/lacz Insertion Library was prepared in pHSSG-Sal; genomic DNA library was prepared in pHSSG-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This
Saccharomycetales; Saccharomycetaceae; Saccharomycetes; (bases 1 to 537)
Rosss-Macdonald, P., Roemer, T. Coelho, P.S. R., Agarwal, S., Kumar, A., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Jansen, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M., Miller, P., Roeder, G.S. and Snyder, M. Gerbe, D., Granda, D., Lugo, R., Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS 29-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 GGCTGTGATGCAGCCGGCCAAATCGTAAAGTTGGGCCCAAATGTTGATGCTGCACGCTTT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AAGGTTGGAGATACCGGTTTTGGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQS02797 1nn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGTCTCAGTTCCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.2%; Score 125; DB 28; Length 537; ilarity 64.4%; Pred. No. 2.9e-20; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Saccharomyces cerevisiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te of mTn-3xHA/lac2 insertion.
Seg primer: GGCTTCTTTTTGGAAGTAC
Class: transposon-tagged.
Location/Qualifiers
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120 TGCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAAT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 TAACTIVAACTCACTCAACTGCTGATGAAATTTCTGAAGGCCCTGTGAAGAACTTCGAATC 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 AAAGGAGGTTCCTTTGCCACCAATGGGTGAAACCATGTTCTGATTAAGAACACTGCCGT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 CTTGAAGGTTGGAGATACCGGTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 Gracaagcregarcaaagreraegringsreeaegreeeereeereeaeeaeeeee 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 AAATGGTGCATTTGCTGAATATGCCAGGGTTTATCCACCTTTGTTTTAC-----AAGAG 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 TGCTGCATCATTGCCAGTTTCGTTGACAACTGCTGGTGTTAGTTTGTGTCATCACTTGGG 470
                                                                                                                                Kluyveromyces delphensis
Kluyveromyces delphensis
Eukaryota, Pungi; Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Baccharomycetaceae; Kluyveromyces.

1 (bases 1 to 467)
Wong, S., Fares, M.A., Zimmermann, W., Butler, G. and Wolfe, K.H..
Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast Candida glabrata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 TCTAGGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAAT---GCTAGTACTGA 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Kluyveromyces delphensis Random Genomic Library"
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11.1%; Score 123.8; DB 29; Length 467;
Best Local Similarity 57.8%; Pred. No. 5.5e-20;
Matches 262; Conservative 0; Mismatches 182; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Kluyveromyces delphensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wong S
Department of Genetics, Smurfit Institute
Trinity College Dublin
Dublin 2. Ireland
Tel: 353 1 6082319
Fax: 353 1 6798558
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/strain="CBS 2170"
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/clone="KD0613"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: swong@tcd.ie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
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                                    ACCESSION
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/notes_Vector: pHSS6-Sal; A yeast genomic DNA library
(lacking mitochondrial DNA) was prepared in pHSS6-Sal;
genomic DNA was statefractionated (DNA of roughly 2-3 kb
in length) prior to cloning. This library was
mubsequently mutagenized with a mrn_3xHA/lacz
muhiltransposon containing lacz, URA3, and tet resistance."
                                                                                     Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetales, Saccharomycetales, Saccharomyceson Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Lossel Loss
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                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Exar: 203 432 6161
Email: anuj.kumar@yale.edu
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                                    Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
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te of mTn-3xHA/lacZ insertion.
Seg primer: GGCCTTCTTTGGAAGTAC
Class: transposon.tagged.
Location/Qualifiers
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/db_xref="taxon:4932"
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                DNA linear GSS 30-NOV-2001 library ASOAA from strain CLIB 533
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/esis...>94
/note="similar to Saccharomyces cerevisiae c...
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I putative frameshift (s)
similar to Saccharomyces cerevisiae ORF YLR460c
similarity to C.carbonum toxD protein ]"
/widence=not_experimental
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                                               Saccharomyces bayanus, genomic survey sequence
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/strain="CLIB 533"
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/clone="AS0AA012C02"
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10.7%; Score 119; DB 29; Length 946;

Query Match

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AQ873736 1inear GSS 08-NOV-1999 V74El mTn-3xHA/lacZ Insertion Library, strain AB972 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
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Roses-Nacdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,
Gesteages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Janser, R.,
Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,
Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
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Saccharomyces cerevisiae
Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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/strain="ABB72 - trpl r(0) ($288C background)"
/db xref="taxon:4932"
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Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
                                      Indels
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1; Mismatches 161;
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A2926593 540 bp DNA linear GSS 01-APR-2001 476.dis09b12.sl Saccharomyces castellii NRRL Y-12630 Saccharomyces castellii genomic clone 476.dis09b12.sl, genomic survey sequence.
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1 (Dasea 1 to 540)

(Giften, P. F., Hillier, L. W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
                                                                                                                                                                                                                                                                                                                                                                     122 GGTAACCCTACCGATTGGAAACATATTGATTTCAAGATTGGTCCTCAAGGTGCCCTCTTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                        184 GGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTG---ACTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GGCTGTGATGCAGCCGGCCAAATCGTAAAGTTGGGCCCAAATGTTNATGCTGCACGCTTT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 AAGGTTGGAGATACCGGTTTTCGTTTCACCGTGCTTCCCAAACAGAT-CCTAAAAA 299
                                                                                                                                                                                                                                            64 GATGTCTCCAGAATTAAAGGAGGTACAGCCTTGGTGAAGGTTGAGGCTGTGCT 123
                                                                                                                                                                                                                                                                                     62 GNCATTCCAATTCCTGAATTAGAAGAATTTGTTCTAATTAAGACTGTCGCGTTGCC 121
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Saccharomyces castellii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                         4 TCAGTTCCAACCACTCAAAAAGCCGTCATCATTGAAGGTGACAAAGCTGTTGTTAAAACA
                                                                                                                                                                                                2 regarrecagaaaceargaaageegrunrearreaaaaregeaagereraacag
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/organism="Saccharomyces castellii"
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/mol_type="ganomic DNA"
/strain="NRL Y-12630 (CBS 4309)"
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/clone="476.dis09bl2.sl"
/clone lib="Saccharomyces castellii NRRL Y-12630"
/note="Random genomic sequence"
/note="Random genomic sequence"
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                                                                  DB 14; Length 337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Johnston M
Department of Genetics
Washington University Medical School
By Sal 1, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108.4; DB 28; Length
Pred. No. 3.9e-16;
0; Mismatches 106; Indele
                                                                                                           Indels
                                                                Score 115.4; DB 14;
Pred. No. 6.1e-18;
0; Mismatches 111;
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Best Local Similarity 61.9
Matches 172; Conservative
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    75
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    83
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/clone_lib="mTn-3xHa/lacZ Insertion Library, strain AB972"
/note="Vector: pHSS6-Sa1; A yeast genomic DNA library was
prepared in pHSS6-Sa1; genomic DNA was size-fractionated
(DNA of coughly 2-3 kb in length) prior to cloning. This
library was subsequently mutagenized with a mTn-3xHa/lacZ
minitransposon containing lacZ, URA3, and tet resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T38505 337 bp mRNA linear EST 11-JAN-1995 EST104002 S. cerevisiae strain X2180-1A Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                 TICCAATICCTGCATTAGAAGAATTTGITCTAATTTAGACTGICGCCGTTGCCGGTA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATACCGATTGGAAACATATTGATTTCGAGATTGGTCCTCAAGGTGCCCTCTTAGGCT 230
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                                                                                                                                                                                                                                                                                                                                                       Trochganaccarganaccerrerearrenanteaceacerererereaceacea 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drdargcadccdacaarcdraaagrrddcccdaardrrgargcrdcacgcrrrgcca 170
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                                                                                                                                                                                                                                                                                                            8 TICCAACCACTCAAAAAGCCGICATCATIGAAGGIGACAAAGCIGITGITAAAACAGAIG 67
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/clone lib="S. cerevisiae strain X2180-1A"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhof"
                                                                                                                                                                                                                                                                     Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tdbinfo@tdb.tigr.org
For clone availability please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                     Score 117.8; DB 28; Length 542;
Pred. No. 1.8e-18;
0; Mismatches 112; Indels 3;
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
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/strain="X2180-1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA 5' end, mRNA sequence.
T38505
T38505.1 GI:622322
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Best Local Similarity 63.3
Matches 198; Conservative
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Fax: 3018699423
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1 (bener, T., Wellen, P., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
1 Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ501976 354A/lacz Insertion Library Saccharomyces cerevisiae
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/mol_type="genomic DNA"
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/note="vector: pHSS6-Sal; A yeast genomic DNA library
/note="vector: pHSS6-Sal; A yeast genomic DNA library
/note="vector: pHSS6-Sal; A yeast genomic DNA of soughly 2-3 kb
in length) prior to cloning. This library was
subsequently mutagenized with a mIn-3xHA/lacz
minitansposon containing lacz, URA3, and tet resistance.'
is a 95 c 76 g 84 t
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                        120 AGATTTACGGATATTGGACCACAAGGTTCCATTCTTGAGTTGTGACATCGCTGGTCAAAT 179
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Saccharomyces cerevisiae
Saccharomyces cerevisiae
Eukaryota; Fungi; Asccmycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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4.4%; Pred. No. 3.4e-13;
ve 0; Mismatches 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: anuj.kumar@yale.edu
te of mTh-3xHA/LacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.
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161; Conservative
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                                                                                                                                                                                                                                           AGCCACAGATTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCA 1007
                                                                                                                                                                                                                                                                                                                                                  TATGAATATTAAAGTTTTCAGCAACGCCTTAGATGTCCCCAGCTCTCACTGAAGGTAT 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A2926284
476.dio48b07.s1 Saccharomyces castellii NRRL Y-12630 Saccharomyces castellii Genomic clone 476.dio48b07.s1, genomic clone 476.dio48b07.s1, genomic survey sequence.
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Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
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                                                                                                                                     947
                                                                                                                                                                                                                                                                                             AGCCACTATTAAAGCTGTTAAATTTGTTACTCCAAAGATCTTGAATGGTGAAATTCATCA 198
                                                                                                                                                                                                                                                                                                                                                                                                    199 TATTCCAATTAAGATTTACAAGAATGGGTTAAGGGATGTTCCTCAATTGACTGATGATAT 258
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                           CATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTGTATCGTGC 887
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                          CATTAAAGAGGAAGACAGAAGATCTAACGTCAAGATCACGGTACCTTGTTGTATTTATC
                                                                                                                                  ATCTGGTCAAGAAATTCTAATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCATGA
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/db_train="NRL Y-1268"
/clone="476.dic48b07.81"
/clone="11b="Saccharomyces castellii NRRL Y-12630"
/note="Random genomic sequence"
79 c 102 g 102 t
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65.8%; Pred. No. 1.8e-13;
cive 0; Mismatches 99; Indels 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1068 AAAAGAAGGTAAAAACAAAATGTTAAGTATGTTGCCA 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 TAAGAACAATAGAAATTCTGGGGAAAAATTAGTTGCCA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Genetics
Washington University Medical School
BA 8232, 4566 Scott Ave., St. Louis, M
Tel: 314 362 2735
Fax: 314 362 7855
Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
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Best Local Similarity
Matches 204; Conserv
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AZ926284
LOCUS
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VERSION
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AUTHORS
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BZ293919 CGN S74 bp DNA linear GSS 31-OCT-2002 CG0601.rl Candida glabrata Random Genomic Library Candida glabrata
  955 GTTAAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCATCATATGAAT 1014
                                                                                            .015 ATTAAAGTTTTCAGCAACGGCTTAGATGATGTCCCAGCTCTCACTGAAGGTATAAAAGAA 1074
                                                                                                                                                                                                                                                                                                                                                          GSS 01-APR-2001
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Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ACAGATGTCTCAGTTCCAGAATTAAAGGAGGTACAGCCTTGGTGAAGGTTGAGGCTGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 GATAACGTCCCATTACCAGAATTAGAAGATGGGTTTTTATTAGTGAAACCAAAGGCTGTC 468
                                          424 ATAAAATTTATTAAGTTCATCAATCCAAAAATCAATGATGGTGAAATCCACCACATCCCA 365
                                                                                                                                      364 GIGATAGITIACAAGAACGGGITAGATGATATCCCACAGTTACTTGATGATATTAAGCAC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                   A2910225
474.dhz51b06.al Saccharomyces unisporus NRRL Y-1556 Saccharomyces unisporus Genomic clone 474.dhz51b06.al, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces unisporus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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/organism="Saccharomyces unisporus"
/mol type="genomic DNA"
/mol type="genomic DNA"
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/clone="474.dhz51b06.81"
/clone=11b="Saccharomyces unisporus NRRL Y-1556"
/note="Random genomic sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGT 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Genetics
Washington University Medical School
Box 832, 4566 Scott Ave., St. Louis, MO 63110, USA
Tal: 314 362 2735
Fax: 314 362 7855
Email: mi@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers
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                                                                                                                                                                                        1075 GGTAAAAACAAAATGTTAAGTATGTTGCCAGGTTATAA 1113
                                                                                                                                                                                                                 304 GGGAGGAATTCTGGCGAAAAGTTGGTTGCGTCTTGAAA 266
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Pred. No. 5.9e-09;
0; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces unisporus
                                                                                                                                                                                                                                                                                                                                                                                                                                AZ930225
AZ930225.1 GI:13501134
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Best Local Similarity 66.1
Matches 115; Conservative
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BZ293919
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Saccharomyces cerevisiae
Bukaryota; Mungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetacese; Saccharomyces.

1 (bases 1 to 549)
Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehn, A., Symoniatis, D., Jansen, R., Munansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone libe "mTh-lakHA/lacz Insertion Library, strain Y2278" / Clone libe "mTh-lakHA/lacz Insertion Library without z micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutegenized with a mTh-3xHA/lacz minitransposon containing lacz, URA3, and tet resistance.
                                                                                                                                                                                                                                                                                                                                                   AQ876344 1near 549 bp DNA linear GSS 08-NOV-1999 V98D9 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 AACGACGICCCATITGGAACGITIACITIGCCAGCAGCACCCIGAAICAAAGGAAGCCGCC 425
ACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTG---ACTTGAAGGTTG 247
                                            232 ATGCAGCCGGCCAAATCGTAAAGTTGGGCCCAAATGTTGATGTTGCACGCTTTGCCATTG 173
                                                                                                                                         GTGATTACATTTATGGGGTTATTCACGGTGCTTCAGTGAGGTTCCCCTCAAACGGTGCCT 113
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                                                                                            GAGATACCGGTTTTCGTTCACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mol type="genomic DNA"
/strain="Y2278 - S288C background, cir(0) rho(0)"
/db xref="taxon:4932"
/lab host="B. coli"
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Pred. No. 1.4e-11;
0; Mismatches 118; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Saccharomyces cerevisiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seg primer.GGCCTTCTTCTTGGAAGTAC
Class: transposon-tagged.
Location/Qualifiers
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Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., destrages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Hasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roceder, G.S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AACAGATGTCTCAGTTCCAGAATTAAAGGAGGGTACAGCCTTGGTGAAGGTTGAGGCTGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 AAAGGAAGITCCTGICCCAGAATIGCGTGATGGITTTGTTCTAGITAAGAATAGAGCTGT 488
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                                                                     Candida glabrata
Candida glabrata
Eukaryota, Fungil Ascomycota, Saccharomycetes,
Bukaryota, Fungil Ascomycota, Saccharomycetales,
Saccharomycetales, mitosporic Saccharomycetales, Candida.

1 (bases 1 to 574)
Wong, S., Fares, M.A., Zimmermann, W., Butler, G. and Wolfe, K.H.
Evidence from comparative genomics for a complete sexual cycle in
the 'asexual' pathogenic yeast Candida glabrata
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
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genomic clone CG0601, genomic survey sequence.
BZ293919
                                                                                                                                                                                                                                                                           Contact: Wong S
Department of Genetics, Smurfit Institute
Trinity College Dublin
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0; Mismatches 43
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mol_type="genomic DNA"
strain="CBS 138"
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/clone="CG0601"
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AQ501614.1 GI:4707264
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Class: plasmid ends.
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Tel: 353 1 6082319
Fax: 353 1 6798558
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetels;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.

B. (bases 1 to 1146)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
L FESS Lett. 487 (1), 3-12 (2000)
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T3 end of clone BCOAA010F11 of library BCOAA from strain CBS 767 of
Debaryomyces hansenii, genomic survey sequence.
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Genomic exploration of the hemiascomycetous yeasts: 14.
Debaryomyces hansenii var. hansenii
FEBS Lett. 487 (1), 82-86 (2000)
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                                               New Haven, CT 06520-8103, USA
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Yale University
P.O. Box 208103, New Haven, CT 06520-
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mrh-3xkk/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
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Location/Qualifiers
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                                                            Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 ENRY cedex - FRANCE (B-mail :
8 seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzil, Zygoasccharomyces rouxzi,
Saccharomyces kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
angusta, Debaryomyces hansenii, var. marxianus, pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia servitophila,
Candida tropolcalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618 GCATGAAAAGCTTTTAAAGTCTTATGGTGCTGATGATGTCTTTGACTATCATGATGCAGG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 GCATCACGATTTCTTGAAATCGTTAGGTGCTGATGAAGTATTTGATTACCATGACTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             678 CGTTATTGAGCAGAT---CAAATCGAAGTATCCAAACCTGCAACATGTTATTGACGCTGT 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 Térchiréhéckéhinanagahaktregregrégrégrégraktraktracearregaraciér 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     735 GGGAAGCGAAGATAGTATCCCCGAGGCCTATAAAGTCACAGCAGATAGTCTACCTGCCAC 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 Trcchacchachactriccaarcccrarccarccarccaccaccaccatarcaaccarctracc 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to Saccharomyces cerevisiae ORF YBR034c [HMT1; hnRNP methyltransferase]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <2. .>550
/note="similar to Saccharomyces cerevisiae ORF YNL134c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <14. >550
/note="similar to Saccharomyces cerevisiae ORF YCR102c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCCAAGTCGCTAAGCTTGCATATGGTT---TAAAGGTCATTACAACCGCATCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity to C.carbonum toXD gene ]
similar to Saccharomyces cerevisiae ORF YLR460c
similarity to C.carbonum toXD protein ]"
//evidence-enct_experimental
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9
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                                                                                                                                                                                                                                                                                                                                                                                                     organism="Debaryomyces hansenii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon:4959"
/clone="BCOAA010F11"
/clone=lib="BCOAA"
/note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA'
/strain="CBS 767"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variety="hansenii"
  (bases 1 to 1146)
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153; Conservative
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Direct Submission
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Best Local (
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BQ143479 556 bp mRNA linear EST 24-APR-2002 fmhlc.pk005.p23 Metarhizium anisopliae sf. acridum ARSEF 324 Metarhizium anisopliae var. acridum cDNA, mRNA sequence.

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BIS16433 SIS Bee Brain Normalized Library, BB16 Apis mellifera cDNA clone BB160022A20C02 5', mRNA sequence.
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                                                                                                                                                                                1 (bases 1 to 556)
Retainoser,F.M., Sorren,S., Baga,S., Hu,G. and St. Leger,R.J.
EST analysis of genes expressed by two different insect pathogenic
fungi during optimized secretion of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Metarhizium anisopliae sf. acridum ARSEF 324"
/note="Vector: Unizap; Metarhizium anisopliae sf. acridum
was grwon on insect curis and chitin for 24 hours. A
cDNA library was constructed in the unidirectional Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 grgacroscocaccaccacracaagaarriccscccaagcroaaaaagcarrcaaarra 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 GAGATACCGGTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAATGGTGCAT 307
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                                                            Metarhizium anisopliae var. acridum
Metarhizium anisopliae var. acridum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
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                                                                                                                                                                                                                                                                                                                       Department of Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA
Tel: 301 405 16 13
Fax: 301 314 92 90
Email: ff34@umail.umd.edu.
Location/Qualifiers
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    .556
    /organism="Metarhizium anisopliae var. acridum"

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4.7%; Score 52.2; DB 13;
Best Local Similarity 53.4%; Pred. No. 0.041;
Matches 133; Conservative 0; Mismatches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:92637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="ARSEF 324"
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Apis mellifera
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EST.
                                                                                                                                                                                                                                                                                                    Contact: Freimoser F. M.
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                     GI:20280538
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                                                                                                                                                                                                                                                                     Email: generobiolife.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR PRimers
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Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.
Annocated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 GAACGTCATTATGGAGGTTTGACTGGTTTAAATAAAGCTGAAACTGCTGCTGAAATATGGT 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Bee Brain Normalized Library, BBL6"
/clone="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
Site_2: Not1; The BBL6 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups. "
74 C 89 g 153 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mkNA"
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.m. ligustica"
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0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev stage="adult worker honey bee"
/lab_host="DH108"
                                                                                                                                              Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Fax: 217 265 0309
Fax: 217 244 3499
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                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: TAATACCACTACTATAGGG
BACKWARD: ATTAACCCTACTAAAB
Plate: BBL60022A20 row: C column: C
Seq primer: AGCGGATAACAATTCACACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Apis mellifera"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 515.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="BB160022A20C02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%;
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BP099113 Chaetomium cDNA library Chaetomium globosum cDNA clone high chaeb.Contig224, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AAGACGGTACCCCTCCCCAGAGCTCCCGGATGACTACATCCTCGTCCGCACCACGGCCGTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GCTGGTAACCCAACTGATTGGAAGCATATTGCTTATAAGATTGGTCCAGAAGGTTCAATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CTAGGATGTGACATTGCTGGTACAGTTGTCAAACTTGGACCAAATGCTAGTACTGACTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AAGGTTGGAGATACCGGTTTTCGGTTTTGTTCACGGTGCTTCCCAAACAGATCCTAAAAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 GTAGGCTGCGACTACGCCGGCATCGTCGAGCAAGTCGGGCCCAAAGTGAACAAGCCCTTC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 AAAAAGGGTGACCGTATCTGCGGAATTGTCCACGGAGCCAACTCGCTGCGGCCTGATGGC 356
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                                                                                                                                                                  Chaetomium globosum
Chaetomium globosum
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Apis mellifera
Apis mellifera
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                         Sordariomycetidae, Sordariales, Chaetomiaceae, Chaetomium 1 (bases 1 to 595)
Yang, Q. and Jin, H.
Chaetomium mycelium EST
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                                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Qian Yang
Contact: Qian Yang
Contact: Qian Yang
Contact: Qian Yang
Contact: Qian Yang
Contact: Qian Yang
Harbin Institute of Technology
West dazhi 92, Harbin, Heilongjiang 150001, China
Fax: 86-451-563-8236
Fax: 86-451-641-2952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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/dev_stage="mycelium"
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Pred. No. 0.058;
0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Chaetomium globosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kimhongseng@x263.net.
Location/Qualifiers
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                                                                                                              BP099113.1 GI:27438553
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BI505803.1 GI:15356177
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Best Local Similarity 47.5%;
Matches 153; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Site_2: Not1; This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 217 265 0309

Fax: 217 24 3499

Fax: 217 24 3499

Email: generobialife uiuc.edu

This research was funded by the University of Illinois Critical

Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation

Award in Functional Genomics to G.E. Robinson and an NSF

Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                                                                                                                                                                                BISO3620
BB170018A20E07.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera CDNA clone BB170018A20E07 5', mRNA sequence.
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(bases 1 to 657)

Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
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/strain="mixed strains of European bees, predominantly
A.m. ligustica"
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91 c 114 g 197 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact; Gene B. Robinson
Department of Entenmology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.6%; Score 51.6; DB 12; Best Local Similarity 52.8%; Pred. No. 0.06; Matches 134; Conservative 0; Mismatches 119;
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BACKWARD: ATTAACCCTCACTAAAG
Plate: BB170018A20 row: E column: 0
Seq primer: AGCGGATAACAATTCACACAGGA
High quality sequence stop: 657.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:7460"
/clone="BB170018A20E07"
                                                                                                                                                                                                                                                                                                                                                           Apis mellifera (honeybee)
                                                                                                                                                                                                                                                                                                        BI503620.1 GI:15353994
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              Apis mellifera
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KEYWORDS
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                                                                                                                                                                                                        DEFINITION
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BI503620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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/note="Organ: brain: Vector: pT713-Pac; Site 1: Ecosl;
Site_2: Not1; This BB17 cDNA library was generated by
subtraction of the BB16 library with 4000 previously
sequenced clones. The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.P., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806, RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: generobiolife.uluc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
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                                                              1 (bases 1 to 619)
Whiffield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Whiffield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 AAATTCACTTTGATATTGCTCATACATCATTATTATCAAGGCTCAAGATACTCTTAAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACGICATTATGGAGGITTGACTGGTTTAAATAAAGCTGAAACTGCTGCTAAATATGGT 337
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Apis mellifera"
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/strain="mixed strains of European bees, predominantly
A.m. ligustica"
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Pred. No. 0.059;
0; Mismatches 119; Indels 1.
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85 c 111 g 178 t
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/dev_stage="adult worker honey bee"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                   505 S. Goddwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
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BACKWARD: ATTAACCCTCACTAAAG
Blate: BB170024A10 TOW: H column: 01
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 619.
Location/Qualiflers
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/clone="BB170024A10H01"
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                                                                                                                                                                                                                                                                                                  Contact: Gene E. Robinson
Department of Entomology
University of Illinois
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Matches 134; Conservative
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Email: generobielife.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BISO4612 669 bp mRNA linear EST 08-APR-2002 BB170025B10C09.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170025B10C09 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 669)
Whiffield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Whiffield, C.W., Band, M.R., Soares, B. and Robinson, G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
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Apis mellifera
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
                                       normalized
sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "

1 cliprosections of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second
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                                                                                                                                                                                                                                                                                                                                           Length 657;
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                                                                                                                                                                                                                                                                                                                                       4.6%; Score 51.6; DB 12;
llarity 52.8%; Pred. No. 0.06;
Conservative 0; Mismatches 119;
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Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: TAATACCACTATAGGG
BACKWARD: ATTAACCTCACTAAAG
Blate: BB170025B10 row: C column: 09
Seq primer: AGCGATAACAATTCACACAGA
High quality sequence stop: 669.
Location/Qualifiers
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351 GATCATAAATATTA 364
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Fax: 217 244 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apidae; Apis.
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 134; Conserv
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Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
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BB170014B20A07.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170014B20A07 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                              GAAGCCACAGTT-AAATTCGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCA 1004
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1 (bases 1 to 657)

1 (bases 1 to 657)

Pardinas, J. Robertson, H.M., Soares, B. and Robinson, G.E.

Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.

Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee

Genome Res. 12 (4), 555-566 (2002)
                                                                                                                                                                                                                                                                                                231 GAACGICATTÁTGGAGGITTÍGACTGGITTAÁATÁAAGCTGAAACTGCTGCTAÁATÁTGGT 290
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111 AAATTCACTTTTGATATTGCTCATACATCATTATTATCAAGGGCTCAAGATACTCTTAAA 170
                                                                          826 AGCATTCCTGAAGAAATCAGAAAAGATAATGTTAAAATTGATATTACTTTGTTGTATCGT 885
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Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
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/strain="mixed strains of European bees, predominantly
                                                                                                                                                171 GCAATTCTTAAAGAAATAGGACAAGAAAACATTACTGTTCAAAAGACATGGCGATTAAAT
                                                                                                                                                                                                                          GCATCTGGTCAAGAATTCTATTGGGTGCAACAAGATTTCCTGCTAGTCCAGAATATCAT
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/dev_stage="adult worker honey bee"
/lab_host="DH10B"
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Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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BACKWARD: ATTAACCCTCACTAAAG
Place: BB170014B20 row: A column: 0
Seq primer: AGCGGATAACAATTACACACAGGA
High quality sequence stop: 657.
Location/Qualifiers
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/db_xref="taxon:7460"
/clone="BB170014B20A07"
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SOURCE
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TITLE

COMMENT

VERSION

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Soarse laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soarse,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                946 GAAGCCACAGTI-AAATICGTTAAGTTTATAAATCCACACCTTAACAACGGTGATATCCA 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           766 AAAGTCACAGCAGATAGTCTACCTGCCACATTATTAGAAGTGGTTCCAATGACCATTGAA 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AAATTCACTTTTGATATTGCTCATACATCATTATTATCAAGGCTCAAGATACTCTTAAA 213
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/drain=refica"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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Pred. No. 0.061;
0; Mismatches 119; Indels 1:
                                                                                                                                                                          /sex="female"
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